



Title	Isolation And Characterization Of The Precursor Virus Of Human Sars Virus: Sars-Associated Corona Virus-Like Virus
Inventor(s)	Guan, Yi; Zheng, Bo Jian
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Guan et al.

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(54) **ISOLATION AND CHARACTERIZATION OF
THE PRECURSOR VIRUS OF HUMAN SARS
VIRUS: SARS-ASSOCIATED CORONA
VIRUS-LIKE VIRUS**

FOREIGN PATENT DOCUMENTS

WO WO 200166689 A2 * 9/2001

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(75) Inventors: **Yi Guan**, Hong Kong (CN); **Bo-Jiang
Zheng**, Hong Kong (CN)

Primary Examiner—Bruce R. Campbell

Assistant Examiner—Louise Humphrey

(73) Assignee: **The University of Hong Kong**, Hong
Kong (CN)

(74) *Attorney, Agent, or Firm*—Saliwanchik, Lloyd &
Saliwanchik

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patent is extended or adjusted under 35
U.S.C. 154(b) by 506 days.

(57) **ABSTRACT**

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(60) Provisional application No. 60/473,255, filed on May
22, 2003.

(51) **Int. Cl.**
C07H 21/02 (2006.01)
C07H 19/00 (2006.01)

(52) **U.S. Cl.** **536/23.1**; 536/23.72

(58) **Field of Classification Search** None
See application file for complete search history.

(56) **References Cited**

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The present invention relates to isolation and characteriza-
tion of a class of isolated novel viruses which is the
precursor of the virus causing Severe Acute Respiratory
Syndrome (SARS) in humans ("hSARS virus"). The pre-
cursor virus which is a SARS coronavirus-like virus
("SCoV-like virus") is identified to be morphologically and
phylogenetically similar to hSARS virus. The present inven-
tion relates to a nucleotide sequence comprising the genomic
sequence of the SCoV-like virus. The invention further
relates to nucleotide sequences comprising a portion of the
genomic sequence of the SCoV-like virus. The invention
also relates to the deduced amino acid sequences of the
SCoV-like virus. The invention further relates to the nucleic
acids and peptides encoded by and/or derived from these
sequences and their use in diagnostic methods and thera-
peutic methods. The invention further encompasses chi-
meric or recombinant viruses encoded by said nucleotide
sequences and antibodies directed against polypeptides
encoded by the nucleotide sequences. Furthermore, the
invention relates to vaccine preparations comprising the
SCoV-like virus, including recombinant and chimeric forms
of said virus.

5 Claims, 82 Drawing Sheets

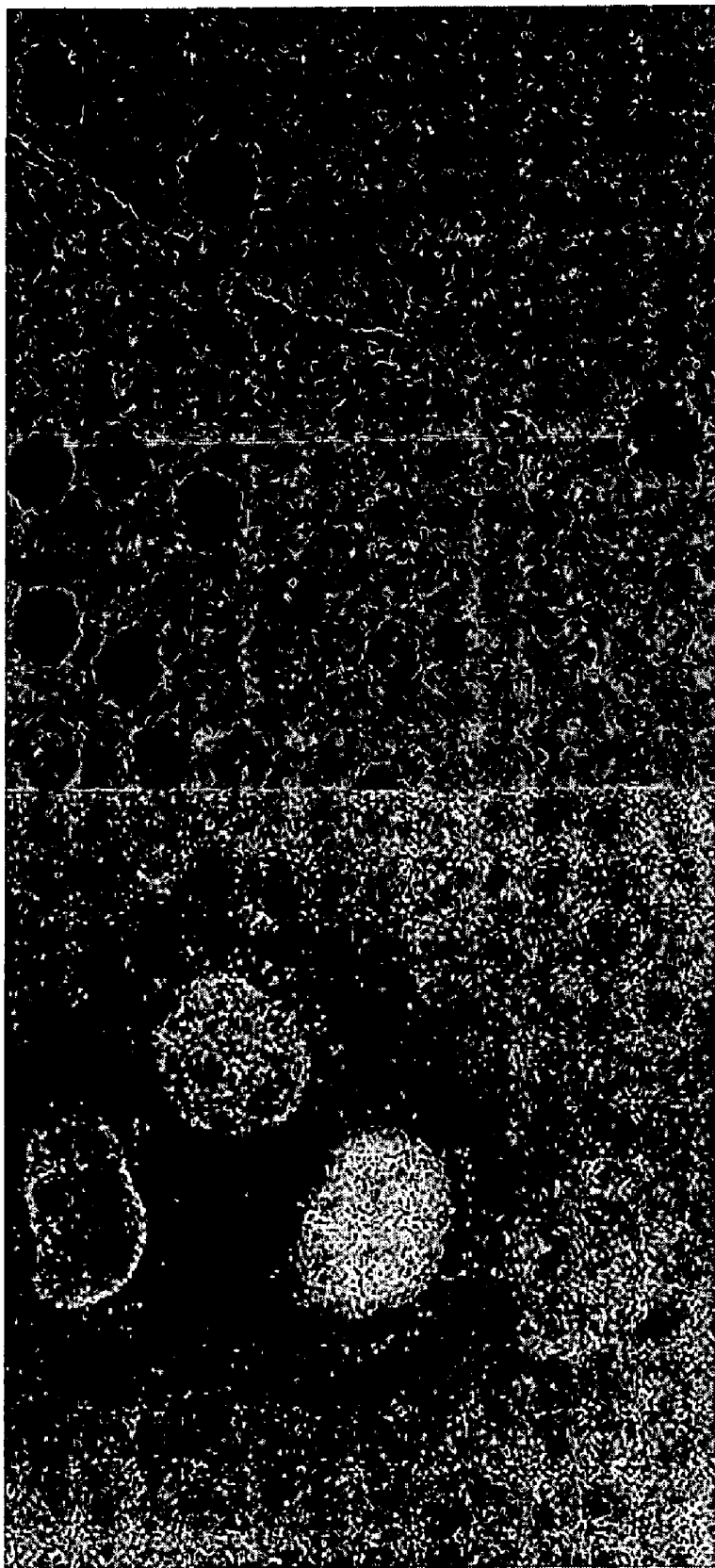


FIG. 1B

FIG. 1A

5'-CCTACTGGTTACCAACCTGAATGGAATAT-3'

FIG. 2

1	ctacccagga	aaagccaacc	aacctcgatc	tcttgtagat	ctgttctcta	aacgaacttt
61	aaaatctgtg	tagctgtcgc	tcggctgcat	gcctagtga	cctacgcagt	ataaacaata
121	ataaatTTtTa	ctgtcgttga	caagaaacga	gtaactcgtc	cctcttctgc	agactgctta
181	cggtttcgtc	cgtgttgag	tcgatcatca	gcatacctag	gtttcgtccg	ggtgtgaccg
241	aaaggtaaga	tggagagcct	tgttcttggt	gtcaacgaga	aaacacacgt	ccaactcagt
301	ttgcctgtcc	ttcaggttag	agacgtgcta	gtgcgtggct	tcggggactc	tgtggaagag
361	gccctatcgg	aggcacgtga	acacctcaaa	aatggcactt	gtggtctagt	agagctggaa
421	aaaggcgtac	tgccccagct	tgaacagccc	tatgtgttca	ttaaacgttc	tgatgcctta
481	agcaccaatc	acggccacaa	ggtcgttgag	ctggttgag	aaatggacgg	cattcagtac
541	ggctgtagcg	gtataacact	gggagtactc	gtgccacatg	tgggcgaaac	cccaattgca
601	taccgcaatg	ttcttcttcg	taagaacggt	aataaggag	ccggtggtca	tagctatggc
661	atcgatctaa	agtcttatga	cttaggtgac	gagcttgga	ctgatcccat	tgaagattat
721	gaacaaaact	ggaacactaa	gcattggcag	ggtgcactcc	gtgaactcac	tcgtgagctc
781	aatggagggtg	cagtcactcg	ctatgtcgac	aacaatttct	gtggcccaga	tgggtaccct
841	cttgattgca	tcaaagattt	tctcgacgc	gcgggcaagt	caatgtgcac	tctttccgaa
901	caacttgatt	acatcgagtc	gaagagaggt	gtctactgct	gccgtgacca	tgagcatgaa
961	attgcctggt	tcactgagcg	ctctgataag	agctacgagc	accagacacc	cttcgaaatt
1021	aagagtgcc	agaaatttga	cactttcaaa	ggggaatgcc	caaagtttgt	gtttcctctt
1081	aactcaaaag	tcaaagtcac	tcaaccacgt	gttgaaaaga	aaaagactga	gggtttcatg
1141	gggcgtatac	gctctgtgta	ccctgttgca	tctccacagg	agtgaacaa	tatgcacttg
1201	tctaccttga	tgaatgtaa	tcattgcgat	gaagtttcat	ggcagacgtg	cgactttctg
1261	aaagccactt	gtgaacattg	tggcactgaa	aatttagtta	ttgaaggacc	tactactagt
1321	gggtacctac	ctactaatgc	tgtagtga	atgccatgtc	ctgcctgtca	agaccagag
1381	attggacctg	agcatagtgt	tgcagattat	cacaaccact	caaacattga	aactcgactc
1441	cgcaaggag	gtaggactag	atgttttga	ggctgtgtgt	ttgcctatgt	tggctgctat
1501	aataagcgtg	cctactgggt	tcctcgtgct	agtgtgata	ttggctcagg	ccatactggc
1561	attactgggt	acaatgtgga	gaccttgaat	gaggatctcc	ttgagatact	gagtcgtgaa
1621	cgtgttaaca	ttaacattgt	tggcgatttt	catttgaatg	aagagggtgc	catcattttg
1681	gcattcttct	ctgcttctac	aagtgccttt	attgacacta	taaagagtct	tgattacaag
1741	tctttcaaaa	ccattgttga	gtcctgcggt	aactataaag	ttaccaaggg	aaagcccgt
1801	aaagggtgct	ggaacattgg	acaacagaga	tcagttttaa	caccactgtg	tgggtttccc
1861	tcacaggctg	ctgggtgttat	cagatcaatt	tttgcgcgca	cacttgatgc	agcaaaccac
1921	tcaattcctg	atttgcaaag	agcagctgtc	accatacttg	atgggtatttc	tgaacagtca
1981	ttacgtcttg	tcgacgccat	ggtttatact	tcagacctgc	tcaccaacag	tgtcattatt
2041	atggcatatg	taactgggtg	tcttgtacaa	cagacttctc	agtgggtgtc	taactctttg
2101	ggcactatg	ttgaaaaact	caggcctatc	tttgaatgga	ttgaggcgaa	acttagtgca
2161	ggagtgtga	ttctcaagga	tgttgggag	attctcaaat	ttctcattac	aggtgttttt
2221	gacatcgtca	aggggtcaaat	acagggtgct	tcagataaca	tcaaggattg	tgtaaaatgc
2281	ttcattgatg	ttgttaacaa	ggcactcgaa	atgtgcattg	atcaagtcac	tatcgctggc
2341	gcaaagtgtg	gatcactcaa	cttaggtgaa	gtcttcatcg	ctcaaagcaa	gggactttac
2401	cgtcagtgtg	tacgtggcaa	ggagcagctg	caactactca	tgcctcttaa	ggcaccacaa
2461	gaagtaacct	ttcttgaagg	tgattcacat	gacacagtac	ttacctctga	ggagggttgt
2521	ctcaagaacg	gtgaactcga	agcactcgag	acgcccgttg	atagcttcac	aaatggagct
2581	atcgttggca	caccagtctg	tgtaaatggc	ctcatgctct	tagagattaa	ggacaaagaa
2641	caatactgcg	cattgtctcc	tggtttactg	gctacaaaca	atgtctttcg	cttaaaaggg
2701	ggtgcaccaa	ttaaagggtg	aaccttttga	gaagatactg	tttgggaagt	tcaagggttac
2761	agaatgtgga	gaatcacatt	tgagcttgat	gaacgtgttg	acaaagtgtc	taatgaaaag
2821	tgtctgtctc	acactgttga	atccggtacc	gaagtacttg	agtttgcatg	tgtttagtga
2881	gaggctgttg	tgaagacttt	acaaccagtt	tctgatctcc	ttaccaacat	gggtattgat
2941	cttgatgagt	ggagtgtagc	tacattctac	ttatttgatg	atgctggtga	agaaaacttt
3001	ctatcacgta	tgtattgttc	cttttaccct	ccagatgagg	aagaagagga	cgatgcagag
3061	tgtgaggaag	aagaaattga	tgaacactgt	gaacatgagt	acggtacaga	ggatgattat
3121	caaggctctc	ctctggaatt	tgggtgctca	gctgaaacag	ttcgagttga	ggaagaagaa
3181	gaggaagact	ggctggatga	tactactgag	caatcagaga	ttgagccaga	accagaacct
3241	acacctgaag	aaccagttaa	tcagtttact	ggttatttaa	aacttactga	caatgttgcc

FIG. 3

3301 attaaatgtg ttgacatcgt taaggaggca caaagtgcta atcctatggt gattgtaaat
3361 gctgctaaca tacacctgaa acatggtggt ggtgtagcag gtgcactcaa caaggcaacc
3421 aatggtgcc a tgcaaaagga gagtgaatgat tacattaagc taaatggccc tcttacagta
3481 ggaggggtc ttttgccttc tggacataat cttgctaaga agtgtctgca tgttgttgga
3541 cctaacctaa atgcaggtga ggacatccag cttcttaagg cagcatatga aaatttcaat
3601 tcacaggaca tcttacttgc accattgttg tcagcaggca tatttggtgc taaaccactt
3661 cagtctttac aagtgtgcgt gcagacggtt cgtacacagg tttatattgc agtcaatgac
3721 aaagctcttt atgagcagg tgtcatggat tatcttgata acctgaagcc tagagtggaa
3781 gcaccta aagaggagcc accaaacaca gaagattcca aaactgagga gaaatctgtc
3841 gtacagaagc ctgtcgatgt gaagccaaaa attaaggcct gcattgatga ggttaccaca
3901 acactggaag aaactaagtt tcttaccat aagttactct tgtttgctga tatcaatggt
3961 aagctttacc atgattctca gaacatgctt agaggtgaag atatgtcttt ccttgagaag
4021 gatgcacctt acatggtagg tgatgttctc actagtgttg atatcacttg tgttgtaata
4081 cctccaaaa aggctggtgg cactactgag atgctctcaa gagctttgaa gaaagtgcc
4141 gttgatgagt atataaccac gtaccctgga caaggatgtg ctgggtatag acttgaggaa
4201 gctaagactg ctcttaagaa atgcaaatct gcattttatg tactaccttc agaagcactt
4261 aatgctaagg aagagattct aggaactgta tcttggaatt tgagagaaat gcttgctcat
4321 gctgaagaga caagaaaatt aatgcctata tgcattgatg ttagagccat aatggcaacc
4381 atccaacgta agtataaagg aattaaaatt caagagggca tcgttgacta tgggtgtccga
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4561 gctgcgcgct gtatgcgttc tcttaaaagc cctgccgtag tgtcagtatc atcaccagat
4621 gctgttacta catataatgg atacctcact tgcgtatcaa agacatctga ggagcacttt
4681 gtagaacacag tttctttggc tggctcttac agagattgggt cctattcagg acagcgtaca
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4861 tccctgcggg aggttaagac tataaaagtg ttcacaactg tggacaacac taatctccac
4921 acacagcttg tggatatgtc tatgacatat ggacagcagt ttgggtccaac atacttggat
4981 ggtgctgatg ttacaaaaat taaacctcat gtaaactcat agggtaagac tttctttgta
5041 ctacctagtg atgacacact acgtagtga gctttcgagt actaccatac tcttgatgag
5101 agttttcttg gtaggtacat gtctgcttta aaccacacaa agaaatggaa atttcctcaa
5161 gttggtgggt taacttcaat taaatgggct gataacaatt gttatttgc tagtgtttta
5221 ttagcacttc aacagcttga agtcaaatc aatgcaccag cacttcaaga ggcttattat
5281 agagcccggtg ctggtgatgc tgctaacttt tgtgcactca tactcgctta cagtaataaa
5341 actgttggcg agcttgggtga tgcagagaa actatgaccc atcttctaca gcatgctaata
5401 ttggaatctg caaagcgagt tcttaatgtg gtgtgtaaac attgtggtca gaaaactact
5461 acctaacgg gtgtagaagc tgtgatgtat atgggtactc tatcttatga taatcttaag
5521 acaggtgttt ccattccatg tgtgtgtggt cgtgatgcta cacaatatct agtaacaaa
5581 gagtcttctt ttgttatgat gtctgcacca cctgctgagt ataaattaca gcaagggtaca
5641 ttcttatgtg cgaatgagta cactggtaac tatcagtgtg gtcattacac tcatataact
5701 gctaaggaga ccctctatcg tattgacgga gctcacctta caaagatgtc agagtacaaa
5761 ggaccagtga ctgatgtttt ctacaaggaa acatcttaca ctacaaccat caagcctgtg
5821 tcgtataaac tcgatggagt tacttacaca gagattgaac caaaattgga tgggtattat
5881 aaaaaggata atgcttacta tacagagcag cctatagacc ttgtaccaac tcaaccatta
5941 ccaaatgcga gttttgataa tttcaaaact acatgttcta acacaaaatt tgcgtatgat
6001 ttaaatcaaa tgacaggctt caaaaagcca gcttcacgag agctatctgt cacattcttc
6061 ccagacttga atggcgatgt agtggctatt gactatagac actattcagc gagtttcaag
6121 aaaggtgcta aattactgca taagccaatt gtttggcaca ttaaccaggc tacaaccaag
6181 acaacgttca aaccaaacac ttggtgttta cgttgtcttt ggagtacaaa gccagtagat
6241 acttcaaat catttgaagt tctggcagta gaagacacac aaggaatgga caatcttgct
6301 tgtgaaagtc aacaaccac ctctgaagaa gtagtggaat atcctaccat acagaaggaa
6361 gtcataagtg gtgacgtgaa aactaccgaa gttgtaggca atgtcatac taaaccatca
6421 gatgaagggt ttaaaagtaac acaagagtta ggtcatgagg atcttatggc tgccttatgtg
6481 gaaaaacacaa gcattaccat taagaaacct aatgagcttt cactagcctt aggtttaaaa
6541 acaattgcc a ctcatggtat tgctgcaatt aatagtgttc cttggagtaa aattttggct

FIG. 3 CONT'D

6601 tatgtcaaac cattcttagg acaagcagca attacaacat caaattgctg taagagatta
6661 gcacaacgtg tgtttaacaa ttatatgcct tatgtgttta cattattggt ccaattgtgt
6721 acttttacta aaagtaccaa ttctagaatt agagcttcac tacctacaac tattgtctaa
6781 aatagtggtta agagtgttg ctaaattatgt ttggatgccg gcattaatta tgtgaagtca
6841 cccaaatttt cttaaattgtt cacaatcgct atgtggctat tgttgtaag tatttgctta
6901 ggttctctaa tctgtgtaac tgctgctttt ggtgtactct tatctaattt tgggtgctct
6961 tcttattgta atggcgtag agaattgtat ctttaattcg ctaacgttac tactatggat
7021 ttctgtgaag gttcttttcc ttgcagcatt tgtttaagt gattagactc ccttgattct
7081 tatccagctc ttgaaacat tcaggtgacg atttcatcg acaagctaga cttgacaatt
7141 ttaggtctgg ccgctgagtg ggttttggca tatatgtgt tcacaaaatt cttttattta
7201 ttaggtcttt cagctataat gcaggtgttc tttggctatt ttgctagtca tttcatcagc
7261 aattcttggc tcatgtggt tatcattagt attgtacaaa tggcaccgt tctgcaatg
7321 gttaggatgt acatcttctt tgcttcttcc tactacatat ggaagagcta tgttcatatc
7381 atggatggt gcacctcttc gacttgcatt atgtgctata agcgcaatcg tgccacacgc
7441 gttgagtgt caactattgt taatggcatg aagagatctt tctatgtcta tgcaaatgga
7501 ggccgtggc tctgcaagac tcacaattgg aattgtctca attgtgacac attttgact
7561 ggttagtcat tcattagtga tgaagttgct cgtgattgt cactccagtt taaaagacca
7621 atcaacccta ctgaccagtc atcgtatatt gttgatagt ttgctgtgaa aaatggcgcg
7681 cttcacctct actttgacaa ggctggctaa aagacctatg agagacatcc tctctccat
7741 tttgtcaatt tagacaatt gagagctaac aacactaaag gttcactgcc tattaatgtc
7801 atagtttttg atggcaagtc caaatgcgac gagtctgctt ctaagtctgc tctgtgtac
7861 tacagtcagc tgatgtgcca acctattctg ttgcttgacc aagctctgt atcagacgtt
7921 ggagatagta ctgaagtttc cgtaagatg tttgatgctt atgtcgacac ctttctagca
7981 acttttagtg ttctatgga aaaacttaag gcacttggtg ctacagctca cagcgagtta
8041 gcaaaggggt tagctttaga tgggtgctct tctacattcg tgtcagctgc ccgacaagg
8101 gttgttgata ccgatgttg cacaaggat gttattgaat gtctcaaact ttcacatcac
8161 tctgacttag aagtgcagg tgacagttgt aacaatttca tgctcaccta taataagggt
8221 gaaaacatga cgcccagaga tcttggcgca tgtattgact gtaatgcaag gcatatcaat
8281 gcccagtgta caaaaagtca caatgttcca ctcattctgga atgtaaaaga ctacatgtct
8341 ttatctgaac agctgcgtaa acaaattcgt agtgctgcca agaagaacaa catacctttt
8401 agactaactt gtgctacaac tagacagggt gtcaatgtca taactactaa aatctcactc
8461 aagggtggt agattgttag tacttgtttt aaacttatgc ttaaggccac attattgtgc
8521 gttcttgctg cattggtttg ttatatcgtt atgccagtac atacattgtc aatccatgat
8581 ggttacacaa atgaaatcat tggttacaaa gccattcagg atggtgtcac tctgtgacac
8641 atttctactg atgattgttt tgcaaataaa catgctggtt ttgacgcatg gtttagccag
8701 cgtggtggt catacaaaaa tgacaaaagc tgccctgtag tagctgctat cattacaaga
8761 gagattggt tcatagtgc ttgcttaccg ggtactgtgc tgagagcaat caatgggtgac
8821 ttcttgcat ttctacctcg tgttttagt gctgttgga acatttgcta cacaccttcc
8881 aaactcattg agtatagtga ttttgctacc tctgcttgcg ttcttgctgc tgagtgtaca
8941 atttttaagg atgctatggg caaacctgtg ccatattgtt atgacactaa tttgtatgag
9001 ggttctatct cttatagtga gcttcgtcca gacactcgtt atgtgcttat ggtgggttcc
9061 atcatacagt ttcctaacac ttacctggag ggttctgtta gtagtagtaac aacttttgat
9121 gctgagtact gtagacatgg tacatgcgaa aggtcagaag taggtatttg cctatctacc
9181 agtggttagat gggttcttaa taatgagcat tacagagctc tatcaggagt tttctgtgg
9241 gttgatgcga tgaatctcat agctaacatc tttactcctc ttgtgcaacc tgtgggtgct
9301 ttagatgtgt ctgcttcagt agtggctggt ggtattattg ccatattggt gacttgtgct
9361 gcctactact ttatgaaatt cagacgtgct tttggtgagt acaaccatgt tgttgctgct
9421 aatgcacttt tgtttttgat gtctttcact atactctgtc tggcaccagc ttacagcttt
9481 ctgccgggag tctactcagt cttttacttg tacttgacat tctatttcac caatgatgtt
9541 tcattcttgg ctcaccttca atggtttgcc atgtttctc ctattgtgcc tttttggata
9601 acagcaatct atgtattctg tatttctctg aagcactgcc attggttctt taacaactat
9661 cttaggaaaa gagtcagtgt taatggagtt acatttagta ccttcgagga ggtgctttg
9721 tgtacctttt tgctcaacaa ggaaatgtac ctaaaattgc gtagcgagac actggttgcca
9781 cttacacagt ataacaggta tcttgctcta tataacaagt acaagtattt cagtggagcc
9841 ttagatacta ccagctatcg tgaagcagct tgctgccact tagcaaaggc tctaaatgac

FIG. 3 CONT'D

9901 ttttagcaact caggtgctga tgttctctac caaccaccac agacatcaat cacttctgct
9961 gttctgcaga gtggttttag gaaaatggca ttcccgtcag gcaaagttga aggggtgcatg
10021 gtacaagtaa cctgtggaac tacaactcct aatggattgt ggttggtatga cacagtatac
10081 tgtccaagac atgtcatttg cacagcagaa gacatgctta atcctaacta tgaagatctg
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10261 acaccaagt ataaatttgt ccgtatccaa cctgggtcaaa cattttcagt tctagcatgc
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10381 ggttctttcc ttaatggatc atgtggtagt gttggtttta acattgatta tgattgctg
10441 tctttctgct atatgcatca tatggagctt ccaacaggag tacacgctgg tactgactta
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10561 acaaccataa cattaaatgt tttggcatgg ctgtatgctg ctgttatcaa tggatgatag
10621 tggtttctta atagattcac cactactttg aatgacttta accttgtggc aatgaagtac
10681 aactatgaac ctttgacaca agatcatgtt gacatattgg gacctcttc tgctcaaaca
10741 ggaattgccg tcttagatat gtgtgctgct ttgaaagagc tgctgcagaa tggatgaat
10801 ggtcgtacta tccttggtag cactatttta gaagatgagt ttacaccatt tgatgttgtt
10861 agacaatgct ctggtgttac cttccaaggt aagttcaaga aaattgttaa gggcactcat
10921 cattggatgc ttttaacttt cttgacatca ctattgatc ttgttcaaag tacacagtgg
10981 tcaactgttt tctttgttta cgagaatgct ttcttgccat ttactcttg tattatggca
11041 attgctgcat gtgctatgct gcttgtaag cataagcac cattcttgtg cttgtttctg
11101 ttaccttctc ttgcaacagt tgcttacttt aatatggtct acatgctgc tagctgggtg
11161 atgcgtatca tgacatggct tgaattggct gacactagct tgtctggtta taggcttaag
11221 gattgtgcta tgtatgcttc agctttagtt ttgcttatcc tcatgacagc ttcgactgtt
11281 tatgatgatg ctgctagacg tgtttggaca ctgatgaatg tcattacact tgtttacaaa
11341 gtctactatg gtaatgcttt agatcaagct atttccatgt gggccttagt tatttctgta
11401 acctctaact attctgggtg cgttacgact atcatgttt tagctagagc tatagtgttt
11461 gtgtgtgttg agtattacc attgttattt attactggca acaccttaca gtgtatcatg
11521 cttgtttatt gtttcttagg ctattgttgc tgctgctact ttggcctttt ctgtttactc
11581 aaccgttact tcaggcttac tcttgggtgt tatgactact tggctctctac acaagaattt
11641 aggtatatga actcccaggg gcttttgctt cctaagagta gtattgatgc tttcaagctt
11701 aacattaagt tgttgggtat tggaggtaaa ccatgtatca aggttgctac tgtacagtct
11761 aaaatgtctg acgtaaagtg cacatctgtg gtactgctct cgttcttcca acaacttaga
11821 gttagatcat cttctaattt gtgggcacaa tgtgtacaac tccacaatga tattcttctt
11881 gcaaaagaca caactgaagc ttctgagaag atggtttctc ttttgtctgt tttgctatcc
11941 atgcagggtg ctgtagacat taatagggtg tgcgaggaat tgctcgataa ccgtgctact
12001 cttcaggcta ttgcttcaga atttagttct ttaccatcat atgcccctta tgccactgcc
12061 caggaggcct atgagcaggc tgtagctaat ggtgattctg aagtcgttct caaaaagtta
12121 aagaaatcct tgaaatgtggc taaatctgag tttgaccgtg atgctgccc gcaacgcaag
12181 ttgaaaaaga tggcagatca ggctatgacc caaatgtaca aacaggcaag atctgaggac
12241 aagagggcaa aagtaactag tgctatgcaa acaatgctct tcaactatgt taggaagctt
12301 gataatgatg cacttaacaa cattatcaac aatgcgcgtg atggttgtgt tccactcaac
12361 atcataccat tgactacagc agccaaactc atggttgttg tccctgatta tggtagctac
12421 aagaacactt gtgatggtaa cacctttaca tatgcatctg cactctggga aatccagcaa
12481 gttgttgatg cggatagcaa gattgttcaa cttagtgaat ttaacatgga caattcacca
12541 aatttggctt ggcctcttat tgttacagct ctaagagcca actcagctgt taaactacag
12601 aataatgaac tgagtccagt agcactacga cagatgtcct gtgcggctgg taccacacaa
12661 acagcttgta ctgatgacaa tgcacttgcc tactataaca attcgaaggg aggtagggtt
12721 gtgctggcat tactatcaga ccaccaagat ctcaaaggg ctgattccc taagagtgt
12781 ggtacaggta caatttacac agaactggaa ccaccttgta ggtttgttac agacacacca
12841 aaagggccta aagtgaataa cttgtacttc atcaaaggct taaacaacct aaatagagg
12901 atggttgctg gcagtttagc tgctacagta cgtcttcagg ctggaaatgc tacagaagta
12961 cctgccaaat caactgtgct ttccttctgt gcttttgca tagacctgc taaagcatat
13021 aaggattacc tagcaagtgg aggacaacca atcaccaact gtgtgaagat gttgtgtaca
13081 cacactggta caggacaggc aattactgta acaccagaag ctaacatgga ccaagagtcc
13141 tttggtgggt cttcatgttg tctgtattgt agatgccaca ttgacctacc aaatcctaaa

FIG. 3 CONT'D

13201	ggattctgtg	acttgaaagg	taagtacgtc	caaataccta	ccacttggtc	taatgaccca
13261	gtgggtttta	cacttagaaa	cacagtctgt	accgtctgcg	gaatgtggaa	aggttatggc
13321	tgtagtgtg	accaactccg	cgaacccttg	atgcagtctg	cggatgcatc	aacgttttta
13381	aacgggtttg	cgggtgtaagt	gcagcccgtc	ttacaccgtg	cggcacaggc	actagtactg
13441	atgtcgtcta	cagggctttt	gatatttaca	acgaaaaagt	tgctgggttt	gcaaagttcc
13501	taaaaactaa	ttgctgtcgc	ttccaggaga	aggatgagga	aggcaattta	ttagactcct
13561	actttgtagt	taagaggcat	actatgtcta	actaccaaca	tgaagagact	atttataact
13621	tggttaaaga	ttgtccagcg	gttgctgtcc	atgacttttt	caagtttaga	gtagatgggtg
13681	acatggtacc	acatatatca	cgtcagcgtc	taactaaata	cacaatggct	gattttagtct
13741	atgctctacg	tcattttgat	gagggtaatt	gtgatacatt	aaaagaaata	ctcgtcacat
13801	acaattgctg	tgatgatgat	tatttcaata	agaaaggattg	gtatgacttc	gtagagaatc
13861	ctgacatctt	acgcgtatat	gctaacttag	gtgagcgtgt	acgccaatca	ttattaaaga
13921	ctgtacaatt	ctgcgatgct	atgcgtgatg	caggcattgt	aggcgtactg	acattagata
13981	atcaggatct	taatgggaac	tggtagcatt	tcggtgattt	cgtacaagta	gcaccaggct
14041	gcggagtccc	tattgtggat	tcataattact	cattgctgat	gcccattctc	actttgacta
14101	gggcattggc	tgctgagtcc	catatggatg	ctgatctcgc	aaaaccactt	attaagtggg
14161	atttgctgaa	atatgatttt	acggaagaga	gactttgtct	cttcgaccgt	tattttaaat
14221	attgggacca	gacataccat	cccaattgta	ttaactgttt	ggatgatagg	tgtatccttc
14281	attgtgcaaa	ctttaatgtg	ttattttcta	ctgtgtttcc	acctacaagt	tttggaccac
14341	tagtaagaaa	aatatattgt	gatggtgttc	cttttgttgt	ttcaactgga	taccattttc
14401	gtgagttagg	agtcgtacat	aatcaggatg	taaacttaca	tagctcgcgt	ctcagtttca
14461	aggaactttt	agtgtatgct	gctgatccag	ctatgcattg	agcttctggc	aattttattgc
14521	tagataaaacg	cactacatgc	ttttcagtag	ctgcactaac	aaacaatgtt	gcttttcaaa
14581	ctgtcaaaac	cggtaatttt	aataaagact	tttatgactt	tgctgtgtct	aaagggtttct
14641	ttaaggaagg	aagttctgtt	gaactaaaac	acttcttctt	tgctcaggat	ggcaacgctg
14701	ctatcagtga	ttatgactat	tatcgttata	atctgccaac	aatgtgtgat	atcagacaac
14761	tcctattcgt	agttgaagtt	gttgataaat	actttgattg	ttacgatggg	ggctgtatta
14821	atgccaacca	agtaatcgtt	aacaatctgg	ataaatcagc	tggtttccca	tttaataaat
14881	ggggtaaggc	tagactttat	tatgactcaa	tgagttatga	ggatcaagat	gcacttttcg
14941	cgtatactaa	gcgtaatgtc	atccctacta	taactcaaat	gaatcttaag	tatgccatta
15001	gtgcaaagaa	tagagctcgc	accgtagctg	gtgtctctat	ctgtagtact	atgacaaata
15061	gacagtttca	tcagaaatta	ttgaagtcaa	tagccgccac	tagaggagct	actgtggtaa
15121	ttggaacaag	caagttttac	ggtggctggc	ataatatgtt	aaaaactggt	tacagtgatg
15181	tagaaactcc	acaccttatg	ggttgggatt	atccaaaatg	tgacagagcc	atgccttaaca
15241	tgcttaggat	aatggcctct	cttgctcttg	ctcgcaaaca	taacacttgc	tgtaacttat
15301	cacaccgttt	ctacaggtta	gctaacgagt	gtgcgcaagt	attaagtgag	atggctcatgt
15361	gtggcggctc	actatatgtt	aaaccagggtg	gaacatcatc	cggatgatgt	acaactgctt
15421	atgctaatag	tgtctttaac	atttgtcaag	ctgttacagc	caatgtaaat	gcacttcttt
15481	caactgatgg	taataagata	gctgacaagt	atgtccgcaa	tctacaacac	aggctctatg
15541	agtgtctcta	tagaaatagg	gatgttgatc	atgaattcgt	ggatgagttt	tacgcttacc
15601	tgcgtaaaaca	tttctccatg	atgattcttt	ctgatgatgc	cgttggtgtc	tataacagta
15661	actatgcggc	tcaaggttta	gtagctagca	ttaagaactt	taaggcagtt	ctttattatc
15721	aaaataatgt	gttcatgtct	gaggcaaaat	gttggactga	gactgacctt	actaaaggac
15781	ctcagaatt	ttgctcacag	catacaatgc	tagttaaaca	aggagatgat	tacgtgtacc
15841	tgccttacct	agatccatca	agaataattag	gcgcaggctg	ttttgtcgat	gatattgtca
15901	aaacagatgg	tacacttatg	attgaaagggt	tcgtgtcact	ggctattgat	gcttaccac
15961	ttacaaaaca	tcctaatacag	gagtatgctg	atgtctttca	cttgatttta	caatacatta
16021	gaaagttaca	tgatgagctt	actggccaca	tgttggacat	gtattccgta	atgctaacta
16081	atgataacac	ctcacggtac	tgggaacctg	agttttatga	ggctatgtac	acaccacata
16141	cagtcttgca	ggctgtagggt	gcttgtgtat	tgtgcaattc	acagacttca	cttcgttgcg
16201	gtgcctgtat	taggagacca	ttcctatggt	gcaagtgtctg	ctatgaccat	gtcatttcaa
16261	catcacacaa	attagtgttg	tctgttaatc	cctatgtttg	caatgcccc	ggttgtgatg
16321	tcactgatgt	gacacaactg	tatctaggag	gtatgagcta	ttattgcaag	tcacataagc
16381	ctcccattag	ttttccatta	tgtgctaattg	gtcagggtttt	tggtttatac	aaaaacacat
16441	gtgtaggcag	tgacaatgtc	actgacttca	atgcgatagc	aacatgtgat	tggactaatg

FIG. 3 CONT'D

16501 ctggcgatta catacttgcc aacacttgta ctgagagact caagcttttc gcagcagaaa
16561 cgctcaaagc cactgaggaa acattttaagc tgtcatatgg tattgccact gtacgcgaag
16621 tactctctga cagagaattg catctttcat gggagggttg aaaacctaga ccaccattga
16681 acagaaacta tgtctttact ggttaccgtg taactaaaaa tagtaaagta cagattggag
16741 agtacacctt tgaaaaaggt gactatggtg atgctgttgt gtacagaggt actacgacat
16801 acaagttgaa tgttggtgat tactttgtgt tgacatctca cactgtaatg ccacttagtg
16861 cacctactct agtgccacaa gagcactatg tgagaattac tggcttgta ccaacactca
16921 acatctcaga tgagttttct agcaatggtg caaattatca aaaggtcggc atgcaaaagt
16981 actctacact ccaaggacca cctgggtactg gtaagagtca ttttgccatc ggacttgctc
17041 tctattaccc atctgctcgc atagtgtata cggcatgctc tcatgcagct gttgatgcc
17101 tatgtgaaaa ggcattaaaa tatttgccca tagataaatg tagtagaatc atacctgcgc
17161 gtgcgcgcgt agagtgtttt gataaattca aagtgaattc aacactagaa cagtatgttt
17221 tctgcactgt aaatgcattg ccagaaacaa ctgctgacat tgtagtcttt gatgaaatct
17281 ctatggctac taattatgac ttgagtgttg tcaatgctag acttcgtgca aaacactacg
17341 tctatattgg cgatcctgct caattaccag ccccccgcac attgctgact aaaggcacac
17401 tagaaccaga atattttta tcaagtgtgca gacttatgaa aacaataggt ccagacatgt
17461 tccttggaac ttgtcgccgt tgcctgctg aaattgttga cactgtgagt gctttagttt
17521 atgacaataa gctaaaagca cacaaggaga agtcagctca atgcttcaaa atgttctaca
17581 aagggtgttat tacacatgat gtttcatctg caatcaacag acctcaataa ggcgttgtaa
17641 gagaatttct tacacgcaat cctgcttgga gaaaagctgt tttatctca ccttataatt
17701 ccagagaacgc tgtagcttca aaaatcttag gattgcctac gcagactgtt gattcatcac
17761 agggttctga atatgactat gtcatattca cacaactac tgaaacagca cactcttgta
17821 atgtcaaccg tttcaatgtg gctatcacaa gggcaaaaat tggcattttg tgcataatgt
17881 ctgatagaga tctttatgac aaactgcaat ttacaagtct agaaatacca cgtcgcaatg
17941 tggctacatt acaagcagaa aatgtaactg gactttttta ggactgtagt aagatcatta
18001 ctggtcttca tcctacacag gcacctacac acctcagcgt tgatataaag ttcaagactg
18061 aaggattatg tgttgacata ccaggcatac caaaggacat gacctaccgt agactcatct
18121 ctatgatggg tttcaaaatg aattaccaag tcaatggtta ccctaatatg tttatcccc
18181 gcgaagaagc tattcgtcac gttcgtgcgt ggattggctt tgatgtagag ggctgtcatg
18241 caactagaga tgctgtgggt actaacctac ctctccagct aggattttct acagggtgta
18301 acttagtagc tgtaccgact ggttatgttg aactgaaaa taacacagaa ttcaccagag
18361 ttaatgcaaa acctccacca ggtgaccagt ttaaaccatct tataccactc atgtataaag
18421 gcttgccctg gaatgtagtg cgtattaaga tagtacaaat gctcagtgat aactgaaaag
18481 gattgtcaga cagagtcgtg ttcgtccttt gggcgcatgg ctttgagctt acatcaatga
18541 agtactttgt caagattgga cctgaaagaa cgtgttgtct gtgtgacaaa cgtgcaactt
18601 gcttttctac ttcacatgat acttatgcct gctggaatca ttctgtgggt tttgactatg
18661 tctataacct atttatgatt gatgttcagc agtggggctt tacgggtaac cttcagagta
18721 acctagacca acattgccag gtacattgaa atgcacatgt ggctagtgtg gatgctatca
18781 tgactagatg tttagcagtc catgagtgtt ttgttaagcg cgttgattgg tctgttgaat
18841 acctatttat aggagatgaa ctgagggtta attctgcttg cagaaaagta caacacatgg
18901 ttgtgaagtc tgcattgctt gctgataagt ttccagttct tcatgacatt ggaaatccaa
18961 aggctatcaa gtgtgtgcct caggctgaag tagaatggaa gttctacgat gctcagccat
19021 gtagtgacaa agcttacaaa atagaggagc tcttctattc ttatgctaca catcacgata
19081 aattcactga tgggtgttgt ttgttttgga attgtaacgt tgatcgttac ccagccaatg
19141 caattgtgtg taggtttgac acaagagtct tgtcaaaact gaacttacca ggctgtgatg
19201 gtggttagtt gtatgtgaat aagcatgcat tccacactcc agctttcgat aaaagtgcac
19261 ttactaattt aaagcaattg cctttctttt actattctga tagtcttgt gagtctcatg
19321 gcaaacaagt agtgtcggat attgattatg ttccactcaa atctgctacg tgtattacac
19381 gatgcaattt aggtggtgct gtttgacagc accatgcaaa tgagtaccga cagtacttgg
19441 atgcatataa tatgatgatt tctgctggat ttagcctatg gatttacaaa caatttgata
19501 cttataacct gtggaatata tttaccaggt tacagagttt agaaaatgtg gcttataatg
19561 ttgttaataa aggacacttt gatggacacg ccggcgaagc acctgtttcc atcatataa
19621 atgctgttta ccaaaaggta gatggtattg atgtggagat ctttgaaaat aagacaacac
19681 ttcctgttaa tgttgcatg gagctttggg ctaagcgtaa cattaaacca gtgccagaga
19741 ttaagatact caataatttg ggtgttgata tgcgtgctaa tactgtaatc tgggactaca

FIG. 3 CONT'D

19801 aaagagaagc cccagcacat gtatctacaa taggtgtctg cacaatgact gacattgcc
19861 agaaacctac tgagagtgtc tttctctcac ttactgtctt gtttgatggg agagtggag
19921 gacaggtaga cttttttaga aacgcccgtg atgggtgttt aataacagaa gggtcagtc
19981 aaggtctaac accttcaaag ggaccagcac aagctagcgt caatggagtc acattaattg
20041 gagaatcagt aaaaacacag ttttaactact ttaagaaagt agacggcatt attcaacagt
20101 tgccatgaaac ctactttact cagagcagag acttagagga ttttaagccc agatcacaaa
20161 tggaaactga ctttctcgag ctgctatgg atgaattcat acagcgatat aagctcgagg
20221 gctatgcctt cgaacacatc gtttatggag atttcagtc tggacaactt ggcggtcttc
20281 atttaatgat aggccttagc aagcgtcac aagattcacc acttaaatta gaggatttta
20341 tccctatgga cagcacagtg aaaaattact tcataacaga tgcgcaaaca gggtcatcaa
20401 aatgtgtgtg ttctgtgatt gatcttttac ttgatgactt tgtcgagata ataaagtcat
20461 aagatttgtc agtgatttca aaagtggcca aggttacaat tgactatgct gaaatttcat
20521 tcatgctttg gtgtaaggat ggacatgttg aaaccttcta cccaaaacta caagcaagtc
20581 aagcgtggca accaggtgtt gcatgacctt acttgtaaca gatgcaaaga atgcttcttg
20641 aaaagtgtga ctttcagaat tatggtgaaa atgctgttat accaaaagga ataatgatga
20701 atgtcgcaaa gtatactcaa ctgtgtcaat acttaatac acttacttta gctgtacctt
20761 acaactgag agttattcac tttggtgctg gctctgataa aggagttgca ccaggtacag
20821 ctgtgctcag acaatggttg ccaactggca cactacttgt cgattcagat cttaatgact
20881 tctgtctccg cgcagattct actttaattg gagactgtgc aacagtacat acggctaata
20941 aatgggacct tattattagc gatattgtat accctaggac caaacatgtg acaaaagaga
21001 atgactctaa agaagggttt ttcacttatc tgtgtggatt tataaagcaa aaactagccc
21061 tgggtggttc tatagctgta aagataacag agcattcttg gaatgctgac ctttacaagc
21121 ttatgggcca tttctcatgg tggacagctt ttgttacaaa tgtaaatgca tcatcatcgg
21181 aagcattttt aattggggct aactatcttg gcaagccgaa ggaacaaatt gatggctata
21241 ccatgcatgc taactacatt ttctggagga acacaaatcc tatccagttg tcttcttatt
21301 cactctttga catgagcaaa tttcctctta aattaagagg aactgctgta atgtctctta
21361 aggagaatca aatcaatgat atgatttatt ctcttctgga aaaaggtagg cttatcatta
21421 gagaaaacaa cagagttgtg gtttcaagtg atattcttgt taacaactaa acgaacatgt
21481 ttattttctt attatttctt actctcacta gtggtagtga ccttgaccgg tgcaccactt
21541 ttgatgatgt tcaagctcct aattacactc aacatacttc atctatgagg ggggtttact
21601 atctgatga aattttttaga tcagacactc tttatttaac tcaggattta tttcttccat
21661 tttattctaa tgttacaggg tttcatacta ttaatcatat gtttgacaac cctgtcatac
21721 cttttaagga tggattttat tttgctgcca cagagaaatc aaatgtgtgc cgtggttggg
21781 tttttggttc taccatgaac aacaagtcac agtcggtgat tattattaac aattctacta
21841 atgttggtat acgagcatgt aactttgaat tgtgtgacaa cccttctttt gctgtttcta
21901 aacccatggg tacacagaca catactatga tattcgataa tgcatttaat tgcactttcg
21961 agtacatatc tgatgccttt tcgcttgatg tttcagaaaa gtcaggtaat tttaaacact
22021 tacgagagtt tgtgtttaa aataaagatg ggtttctcta tgtttataag ggctatcaac
22081 ctatagatgt agttcgtgat ctaccttctg gttttaacac tttgaaacct atttttaagt
22141 tgccctcttg tattaacatt acaaatttta gagccattct tacagccttt tcacctgtct
22201 aagacacttg gggcacgtca gctgcagcct attttggttg ctatttaaag ccaactacat
22261 ttatgctcaa gtatgatgaa aatggtacaa tcacagatgc tgttgattgt tctcaaaatc
22321 cacttgctga actcaaatgc tctgttaaga gctttgagat tgacaaaagga atttaccaga
22381 cctctaattt cagggtgtgt ccctcaggag atgttggtgag attccctaatt attacaact
22441 tctgtccttt tggagaggtt tttaatgcta ctaaaattccc ttctgtctat gcatgggaga
22501 gaaaaaaaaa ttctaattgt gttgctgatt actctgtgct ctacaactca acattttttt
22561 caacctttta gtgctatggc gtttctgcca ctaagttgaa tgatctttgc ttctccaatg
22621 tctatgcaga ttcttttgta gtcaaggag atgatgtaag acaaatagcg ccaggacaaa
22681 ctggtgttat tgctgattat aattataaat tgccagatga tttcatgggt tgtgtccttg
22741 cttggaatac taggaacatt gatgctactt caactggtaa ttataattat aaatataggt
22801 atcttagaca tggcaagctt aggccttttg agagagacat atctaattgt cctttctccc
22861 ctgatggcaa accttgacc ccacctgtct ttaattgtta ttggccatta aatgattatg
22921 gtttttacac cactactggc attggctacc aaccttacag agttgtagta ctttcttttg
22981 aactttttaa tgcaccggcc acggtttgtg gaccaaatt atccactgac cttattaaga
23041 accagtgtgt caattttaat tttaatggac tcactggtac tgggtgtgta actccttctt

FIG. 3 CONT'D

23101 caaagagatt tcaaccatth caacaatttg gccgtgatgt ttctgatttc actgattccg
23161 ttcgagatcc taaaacatct gaaatattag acatttcacc ttgctctttt gggggtgtaa
23221 gtgtaattac acctggaaca aatgcttcat ctgaagttgc tgttctatat caagatgtta
23281 actgcactga tgtttctaca gcaattcatg cagatcaact cacaccagct tggcgcatat
23341 attctactgg aaacaatgta ttccagactc aagcaggctg tcttatagga gctgagcatg
23401 tgcacacttc ttatgagtgc gacattccta ttggagctgg catttggtgt agttaccata
23461 cagtttcttt attacgtagt actagccaaa aatctattgt ggcttatact atgtcttttag
23521 gtgctgatag ttcaattgct tactctaata acaccattgc tatacctact aacttttcaa
23581 ttagcattac tacagaagta atgctgttt ctatggctaa aacctccgta gattgtaata
23641 tgtacatctg cggagattct actgaatgtg ctaatttgct tctccaatat ggtagctttt
23701 gcacacaact aaatcgtgca ctctcaggta ttgctgctga acaggatcgc aacacacgtg
23761 aagtgttcgc tcaagtcaaa caaatgtaca aaaccccaac ttgaaatat tttgggtggt
23821 ttaatttttc acaaattatta cctgaccctc taaagccaac taagagggtct ttatttgagg
23881 acttgctctt taataagggtg acactcgctg atgctggctt catgaagcaa tatggcgaat
23941 gcctaggtga tattaatgct agagatctca tttgtgcgca gaagtccaat ggacttacag
24001 tgttgccacc tctgctcact gatgatatga ttgctgctca cactgctgct ctagttagtg
24061 gtactgccac tgctggatgg acatttggtg ctggcgctgc tcttcaaata ccttttgcta
24121 tgcaaatggc atataggttc aatggcattg gagtaccca aaatgttctc tatgagaacc
24181 aaaaacaaat cgccaaccaa ttaacaagg cgattagtca aattcaagaa tcacttacaa
24241 caacatcaac tgcattgggc aagctgcaag acgttggtta ccagaatgct caagcattaa
24301 acacacttgt taaacaactt agctctaatt ttggtgcaat ttcaagtgtg ctaaatgata
24361 tcctttcgcg acttgataaa gtcgaggcgg aggtacaaat tgacagggtta attacaggca
24421 gacttcaaag ccttcaaacc tatgtaacac aacaactaat cagggtgctg gaaatcaggg
24481 cttctgctaa tcttgctgct actaaaatgt ctgagtgtgt tcttggaaca tcaaaaagag
24541 ttgacttttg tggaaagggc taccacctta tgtccttccc acaagcagcc ccgcatgggtg
24601 ttgtcttctt acatgtcacg tatgtgccat cccaggagag gaacttcacc acagcgccag
24661 caatttgtca tgaaggcaaa gcatacttcc ctctgtaagg tgtttttgtg tttaatggca
24721 cttcttggtt tattacacag aggaacttct tttctccaca aataattact acagacaata
24781 catttgtctc aggaatttgt gatgtcgta ttggcatcat taacaacaca gtttatgatc
24841 ctctgcaacc tgagcttgac tcattcaaag aagagctgga caagtacttc aaaaatcata
24901 catcaccaga tgttgatctt ggcgacattt caggcattaa cgcttctgtc gtcaacattc
24961 aaaaagaaat tgaccgcctc aatgaggctg ctaaaaatth aaatgaatca ctcatgacc
25021 ttcaagaatt gggaaaatat gagcaatata ttaaatggcc ttggtatggt tggctcggct
25081 tcattgctgg actaattgcc atcgtcatgg ttacaatctt gctttgttgc atgactagtt
25141 gttgcagttg cctcaagggt gcattgctct gtggttcttg ctgcaagttt gatgaggatg
25201 actctgagcc agttctcaag ggtgtcaaat tacattacac ataaacgaac ttatggattt
25261 gtttttgaga ttttttactc ttggatcaat tactgcacag ccagtaaaa ttgacaattgc
25321 ttctcctgca agtactgttc atgctacagc aacgataccg ctacaagcct cactcccttt
25381 cggatggctt gttattggcg ttgcatttct tgcgtgtttt cagagcgcta caaaaataat
25441 tgcgtcfaat aaaagatggc agctagccct ttataagggc ttccagttca tttgcaattt
25501 actgctgcta tttgttacca tctattcaca tcttttgctt gtcgctgcag gtatggaggc
25561 gcaatttttg tacctctatg ccttgatata tttctacaa tgcatacaac catgtagaat
25621 tattatgaga tgttggtctt gttggaagtg caaatccaag aaccattac ttatgatgac
25681 caactacttt gtttgctggc acacacataa ctatgactac tgtataccat ataacagtgt
25741 cacagataca attgtcgta ctgaagggtg cggcatttca acacaaaaac tcaagaaga
25801 ctaccaaatt ggtggttatt ctgaggatag gcactcaggt gttaaagact atgtcgttgt
25861 acatggctat ttaccgaag ttactacca gcttgagtct acacaaatta ctacagacac
25921 tggatttgaa aatgctacat tcttcatctt taacaagctt gttaaagacc caccgaatgt
25981 gcaaatacac acaatcgacg gctcttcagg agttgcta at ccagcaatgg atccaattta
26041 tgatgagccg acgacgacta ctacgctgcc tttgtaagca caagaaagtg agtacgaact
26101 tatgtactca ttcgtttcgg aagaaacagg tacgttaata gttaatagcg tacttctttt
26161 tcttgctttc gtggtattct tgctagtac actagccatc cttactgcgc ttcgattgtg
26221 tgcgtactgc tgcaatattg ttaacgtgag tttagtaaaa ccaacgggtt acgtctactc
26281 gcgtgttaaa aatctgaact cttctgaagg agttcctgat cttctgggtc aaacgaacta
26341 actattatta ttattctggt tggaaactta acattgctta tcatggcaga caacgggtact

FIG. 3 CONT'D

26401 attaccgttg aggagcttaa acaactcctg gaacaatgga acctagtaat aggtttccta
26461 ttccctagcct ggattatgtt actacaattt gcctattcta atcggaaacag gttttgttac
26521 ataataaagc ttgttttcct ctggctcctg tggccagtaa cacttgcttg ttttgtgctt
26581 gctgctgtct acagaattaa ttgggtgact ggcgggattg cgattgcaat ggcttgtatt
26641 gtaggcttga tgtggcttag ctacttcgtt gcttccttca ggctgtttgc tcgtaccgcg
26701 tcaatgtggt cattcaaccc agaaacaaac attcttctca atgtgcctct ccgggggaca
26761 attgtgacca gaccgctcat ggaaagtga cttgtcattg gtgctgtgat cattcgtggt
26821 cacttgcgaa tggccggaca ctccttaggg cgctgtgaca ttaaggacct gccaaaagag
26881 atcactgtgg ctacatcacg aacgccttct tattacaaat taggagcgtc gcagcgtgta
26941 ggcactgatt caggttttgc tgcatacaac cgctaccgta ttggaaacta taaattaaat
27001 acagaccacg ccggtagcaa cgacaatatt gctttgctag tacagtaagt gacaacagat
27061 gtttcatctt gttgacttcc aggttacaat agcagagata ttgattatca ttatgaggac
27121 tttcaggatt gctatttggg atcttgacgt tataataagt tcaatagtga gacaattatt
27181 taagcctcta actaagaaga attattcgga gtttagatgat gaagaaccta tggagttaga
27241 ttatccataa aacgaacatg aaaattattc tcttctgac attgattgta tttacatctt
27301 gcgagctata tcaactacag gagtgtgta gaggtacgac tgtactacta aaagaacctt
27361 gcccatcagg aacatacgag ggcaattcac catttcaccc tcttgctgac aataaatttg
27421 cactaacttg cactagcaca cactttgctt ttgcttgtgc tgacgggtact cgacatacct
27481 atcagctgcg tgcaagatca gtttcaccaa aacttttcat cagacaagag gaggttcaac
27541 aagagctcta ctgccactt tttctcattg ttgctgctct agtattttta atactttgct
27601 tcaccattaa gagaaagaca gaatgaatga gctcacttta attgacttct atttgtgctt
27661 tttagccttt ctgctattcc ttgttttaat aatgcttatt atattttggt tttcactcga
27721 aatccaggat ctagaagaac cttgtacca aagtctaaacg aacatgaaac ttctcattgt
27781 tttgacttgt atttctctat gcagttgcat acgcactgta gtacagcgtc gtgcatctaa
27841 taaacctcat gtgcttgaag atccttgtaa ggtacaacac taggggtaat acttatagca
27901 ctgcttggtt ttgtgctcta ggaaagggtt taccttttca tagatggcac actatggttc
27961 aaacatgcac acctaattgtt actatcaact gtcaagatcc agctgggtgt gcgcttagatg
28021 ctaggtgttg gtaccttcat gaaggctacc aaactgctgc atttagagac gtacttgttg
28081 ttttaataa acgaacaaat taaaatgtct gataatggac cccaatcaaa ccaacgtagt
28141 gcccccgca ttacatttg tggaccaca gattcaactg acaataacca gaatggagga
28201 cgcaatgggg caaggccaaa acagcgccga cccaagggtt taccataaa tactgctct
28261 tgggttcacag ctctcactca gcatggcaag gaggaactta gattccctcg aggccagggc
28321 gttccaatca acaccaatag tgggtccagat gaccaaatg gctactaccg aagagctacc
28381 cgacgagttc gtggtggtga cggcaaatg aaagagctca gcccagatg gtacttctat
28441 tacctaggaa ctggccaga agcttcactt ccctacggcg ctaacaaaga aggcactgta
28501 tgggttgcaa ctgagggagc cttgaatata cccaaagacc acattggcac ccgcaatcct
28561 aataacaatg ctgccaccgt gctacaactt cctcaaggaa caacattgcc aaaaggcttc
28621 tacgcagagg gaagcagagg cggcagtcaa gcctcttctc gctcctcctc acgtagtcgc
28681 ggtaattcaa gaaattcaac tcctggcagc agtaggggaa attctcctgc tcgaatggct
28741 agcggaggtg gtgaaactgc cctcgcgcta ttgctgctag acagattgaa ccagcttgag
28801 agcaaaagtt ctggttaaagg ccaacaacaa caaggccaaa ctgtcactaa gaaatctgct
28861 gctgaggcat ctaaaaagcc tcgcaaaaaa cgtactgcca caaacagta caacgtcact
28921 caagcatttg ggagacgtgg tccagaacaa acccaaggaa atttcgggga ccaagacct
28981 atcagacaag gaactgatta caaacattgg ccgcaaatg cacaatttgc tccaagtgc
29041 tctgcattct ttggaatgtc acgcattggc atggaagtca caccttcggg aacatggctg
29101 acttatcatg gagccattaa attggatgac aaagatccac aattcaaaga caacgtcata
29161 ctgctgaaca agcacattga cgcatacaaa acattccac caacagagcc taaaaaggac
29221 aaaaagaaaa agactgatga agctcagcct ttgccgcaga gacaaaagaa gcagccact
29281 gtgactcttc ttctgctggc tgacatggat gatttctoca gacaacttca aaattccatg
29341 agtggagctt ctgctgattc aactcaggca taaacactca tgatgaccac acaaggcaga
29401 tgggctatgt aaacgttttc gcaattccgt ttacgatata tagtctactc ttgtgcagaa
29461 tgaattctcg taactaaaca gcacaagtag gtttagttaa ctttaattct acatagcaat
29521 ctttaatacaa tgtgtaacat tagggaggac ttgaaagagc caccacattt tcatcgaggc
29581 cacgcggagt acgatcgagg gtacagtga taatgctagg gagagctgcc tatatggag
29641 agccctaatt tgtaaaatta attttagtag tgctatcccc atgtgatttt aatagcttct
29701 taggagaatg acaaaaaaaa aaaaaaaaaa aaaaaa

FIG. 3 CONT'D

1 - CTACCCAGGAAAAGCCAACCAACCTCGATCTCTTGTAGATCTGTTCTCTAAACGAACTTT - 60
- L P R K S Q P T S I S C R S V L * T N F
- Y P G K A N Q P R S L V D L F S K R T L
- T Q E K P T N L D L L * I C S L N E L *
61 - AAAATCTGTGTAGCTGTCGCTCGGCTGCATGCCTAGTGCACCTACGCAGTATAACAATA - 120
- K I C V A V A R L H A * C T Y A V * T I
- K S V * L S L G C M P S A P T Q Y K Q *
- N L C S C R S A A C L V H L R S I N N N
121 - ATAAATTTTACTGTCGTTGACAAGAAACGAGTAACCTCGTCCCTCTTCTGCAGACTGCTTA - 180
- I N F T V V D K K R V T R P S S A D C L
- * I L L S L T R N E * L V P L L Q T A Y
- K F Y C R * Q E T S N S S L F C R L L T
181 - CGGTTTCGTCCGTGTTGTCAGTCGATCATACCTAGGTTTCGTCCGGGTGTGACCG - 240
- R F R P C C S R S S A Y L G F V R V * P
- G F V R V A V D H Q H T * V S S G C D R
- V S S V L Q S I I S I P R F R P G V T E
241 - AAAGTAAGATGGAGAGCCTTGTCTTGGTGTCAACGAGAAAACACACGTCCTCAACTCAGT - 300
- K G K M E S L V L G V N E K T H V Q L S
- K V R W R A L F L V S T R K H T S N S V
- R * D G E P C S W C Q R E N T R P T Q F
301 - TTGCCTGTCTTCAGGTTAGAGACGTGCTAGTGCCTGGCTTCGGGGACTCTGTGGAAGAG - 360
- L P V L Q V R D V L V R G F G D S V E E
- C L S F R L E T C * C V A S G T L W K R
- A C P S G * R R A S A W L R G L C G R G
361 - GCCCTATCGGAGGCACGTGAACACCTCAAAAATGGCACTTGTGGTCTAGTAGAGCTGGAA - 420
- A L S E A R E H L K N G T C G L V E L E
- P Y R R H V N T S K M A L V V * * S W K
- P I G G T * T P Q K W H L W S S R A G K
421 - AAAGGCGTACTGCCCCAGCTTGAACAGCCCTATGTGTTTATTAAACGTTCTGATGCCTTA - 480
- K G V L P Q L E Q P Y V F I K R S D A L
- K A Y C P S L N S P M C S L N V L M P *
- R R T A P A * T A L C V H * T F * C L K
481 - AGCACCAATCACGGCCACAAGGTCGTTGAGCTGGTTCAGAAATGGACGGCATTTCAGTAC - 540
- S T N H G H K V V E L V A E M D G I Q Y
- A P I T A T R S L S W L Q K W T A F S T
- H Q S R P Q G R * A G C R N G R H S V R
541 - GGTGCTAGCGGTATAACACTGGGAGTACTCGTGCCACATGTGGGCGAAACCCCAATTGCA - 600
- G R S G I T L G V L V P H V G E T P I A
- V V A V * H W E Y S C H M W A K P Q L H
- S * R Y N T G S T R A T C G R N P N C I
601 - TACCGCAATGTTCTTCTCTGTAAGAACGGTAATAAGGGAGCCGGTGGTCATAGCTATGGC - 660
- Y R N V L L R K N G N K G A G G H S Y G
- T A M F F F V R T V I R E P V V I A M A
- P Q C S S S * E R * * G S R W S * L W H
661 - ATCGATCTAAAGTCTTATGACTTAGGTGACGAGCTTGGCACTGATCCCATTGAAGATTAT - 720
- I D L K S Y D L G D E L G T D P I E D Y
- S I * S L M T * V T S L A L I P L K I M
- R S K V L * L R * R A W H * S H * R L *
721 - GAACAAACTGGAACACTAAGCATGGCAGTGGTGCACCTCCGTGAACTCACTCGTGAGCTC - 780
- E Q N W N T K H G S G A L R E L T R E L
- N K T G T L S M A V V H S V N S L V S S
- T K L E H * A W Q W C T P * T H S * A Q
781 - AATGGAGGTGCAGTCACTCGCTATGTCGACAACAATTTCTGTGGCCAGATGGGTACCCT - 840
- N G G A V T R Y V D N N F C G P D G Y P
- M E V Q S L A M S T T I S V A Q M G T L
- W R C S H S L C R Q Q F L W P R W V P S
841 - CTTGATTGCATCAAAGATTTTCTCGCACGCGCGGCAAGTCAATGTGCACTCTTTCCGAA - 900
- L D C I K D F L A R A G K S M C T L S E
- L I A S K I F S H A R A S Q C A L F P N
- * L H Q R F S R T R G Q V N V H S F R T

FIG. 4

901 - CAACTTGATTACATCGAGTCGAAGAGAGGTGTCTACTGCTGCCGTGACCATGAGCATGAA - 960
- Q L D Y I E S K R G V Y C C R D H E H E
- N L I T S S R R E V S T A A V T M S M K
- T * L H R V E E R C L L L P * P * A * N
961 - ATTCCTGGTTCACTGAGCGCTCTGATAAGAGCTACGAGCACCAGACACCCTTCGAAATT - 1020
- I A W F T E R S D K S Y E H Q T P F E I
- L P G S L S A L I R A T S T R H P S K L
- C L V H * A L * * E L R A P D T L R N *
1021 - AAGAGTGCCAAGAAATTTGACACTTTCAAGGGGAATGCCCAAAGTTTGTGTTTCCTCTT - 1080
- K S A K K F D T F K G E C P K F V F P L
- R V P R N L T L S K G N A Q S L C F L L
- E C Q E I * H F Q R G M P K V C V S S *
1081 - AACTCAAAAGTCAAAGTCATTCAACCAGTGTGAAAAGAAAAAGACTGAGGGTTTCATG - 1140
- N S K V K V I Q P R V E K K K T E G F M
- T Q K S K S F N H V L K R K R L R V S W
- L K S Q S H S T T C * K E K D * G F H G
1141 - GGGCGTATACGCTCTGTGTACCCTGTTGCATCTCCACAGGAGTGTAACAATATGCACTTG - 1200
- G R I R S V Y P V A S P Q E C N N M H L
- G V Y A L C T L L H L H R S V T I C T C
- A Y T L C V P C C I S T G V * Q Y A L V
1201 - TCTACCTTGATGAAATGTAATCATTGCGATGAAGTTTCATGGCAGACGTGCGACTTTCTG - 1260
- S T L M K C N H C D E V S W Q T C D F L
- L P * * N V I I A M K F H G R R A T F *
- Y L D E M * S L R * S F M A D V R L S E
1261 - AAAGCCACTTGTGAACATTGTGGCACTGAAAATTTAGTTATTGAAGGACCTACTACATGT - 1320
- K A T C E H C G T E N L V I E G P T T C
- K P L V N I V A L K I * L L K D L L H V
- S H L * T L W H * K F S Y * R T Y Y M W
1321 - GGGTACCTACCTAATGCTGTAGTGAAAATGCCATGTCCTGCCTGTCAAGACCCAGAG - 1380
- G Y L P T N A V V K M P C P A C Q D P E
- G T Y L L M L * * K C H V L P V K T Q R
- V P T Y * C C S E N A M S C L S R P R D
1381 - ATTGACCTGAGCATAGTGTGCAGATTATCACAACCACTCAAACATTGAAACTCGACTC - 1440
- I G P E H S V A D Y H N H S N I E T R L
- L D L S I V L Q I I T T T Q T L K L D S
- W T * A * C C R L S Q P L K H * N S T P
1441 - CGCAAGGGAGGTAGGACTAGATGTTTTGGAGGCTGTGTGTTTGCCTATGTTGGCTGCTAT - 1500
- R K G G R T R C F G G C V F A Y V G C Y
- A R E V G L D V L E A V C L P M L A A I
- Q G R * D * M F W R L C V C L C W L L *
1501 - AATAAGCGTGCCTACTGGGTTCCCTCGTGTAGTGTGATATTGGCTCAGGCCATACTGGC - 1560
- N K R A Y W V P R A S A D I G S G H T G
- I S V P T G F L V L V L I L A Q A I L A
- * A C L L G S S C * C * Y W L R P Y W H
1561 - ATTACTGGTGACAATGTGGAGACCTTGAATGAGGATCTCCTTGAGATACTGAGTCGTGAA - 1620
- I T G D N V E T L N E D L L E I L S R E
- L L V T M V R P * M R I S L R Y * V V N
- Y W * Q C G D L E * G S P * D T E S * T
1621 - CGTGTAAACATTAACATTGTTGGCGATTTTCATTTGAATGAAGAGGTTGCCATCATTTTG - 1680
- R V N I N I V G D F H L N E E V A I I L
- V L T L T L L A I F I * M K R L P S F W
- C * H * H C W R F S F E * R G C H H F G
1681 - GCATCTTTCTCTGCTTCTACAAGTGCCTTTATTGACACTATAAAGAGTCTTGATTACAAG - 1740
- A S F S A S T S A F I D T I K S L D Y K
- H L S L L L Q V P L L T L * R V L I T S
- I F L C F Y K C L Y * H Y K E S * L Q V
1741 - TCTTTCAAACCATGTTGAGTCTCGGTAACATAAAGTTACCAAGGGAAAGCCCGTA - 1800
- S F K T I V E S C G N Y K V T K G K P V
- L S K P L L S P A V T I K L P R E S P *
- F Q N H C * V L R * L * S Y Q G K A R K

FIG. 4 Cont'd

1801 - AAAGGTGCTTGGAAACATTGGACAACAGAGATCAGTTTAAACACCACTGTGTGGTTTTCCC - 1860
- K G A W N I G Q Q R S V L T P L C G F P
- K V L G T L D N R D Q F * H H C V V F P
- R C L E H W T T E I S F N T T V W F S L
1861 - TCACAGGCTGCTGGTGTATCAGATCAATTTTTCGCGCACACTTGATGCAGCAAACCAC - 1920
- S Q A A G V I R S I F A R T L D A A N H
- H R L L V L S D Q F L R A H L M Q Q T T
- T G C W C Y Q I N F C A H T * C S K P L
1921 - TCAATTCCTGATTGCAAAGAGCAGCTGTCACCATACTTGATGGTATTTCTGAACAGTCA - 1980
- S I P D L Q R A A V T I L D G I S E Q S
- Q F L I C K E Q L S P Y L M V F L N S H
- N S * F A K S S C H H T * W Y F * T V I
1981 - TTACGCTTGTGACGCCATGGTTTATACTTCAGACCTGCTCACCAACAGTGCATTATT - 2040
- L R L V D A M V Y T S D L L T N S V I I
- Y V L S T P W F I L Q T C S P T V S L L
- T S C R R H G L Y F R P A H Q Q C H Y Y
2041 - ATGGCATATGTAACCTGGTGGTCTTGTACAACAGACTTCTCAGTGGTGTCTAATCTTTTG - 2100
- M A Y V T G G L V Q Q T S Q W L S N L L
- W H M * L V V L Y N R L L S G C L I F W
- G I C N W W S C T T D F S V V V * S F G
2101 - GGCCTACTGTTGAAAACTCAGGCCTATCTTTGAATGGATTGAGGCGAAACTTAGTGCA - 2160
- G T T V E K L R P I F E W I E A K L S A
- A L L L K N S G L S L N G L R R N L V Q
- H Y C * K T Q A Y L * M D * G E T * C R
2161 - GGAGTTGAATTTCTCAAGGATGCTTGGGAGATTCTCAAATTTCTCATTACAGGTGTTTTT - 2220
- G V E F L K D A W E I L K F L I T G V F
- E L N F S R M L G R F S N F S L Q V F L
- S * I S Q G C L G D S Q I S H Y R C F *
2221 - GACATCGTCAAGGGTCAAATACAGGTTGCTTCAGATAACATCAAGGATTGTGTAAATGC - 2280
- D I V K G Q I Q V A S D N I K D C V K C
- T S S R V K Y R L L Q I T S R I V * N A
- H R Q G S N T G C F R * H Q G L C K M L
2281 - TTCATGATGTTGTTAACAAGGCACTCGAAATGTGCATTGATCAAGTCACTATCGCTGGC - 2340
- F I D V V N K A L E M C I D Q V T I A G
- S L M L L T R H S K C A L I K S L S L A
- H * C C * Q G T R N V H * S S H Y R W R
2341 - GCAAAGTTGCGATCACTCAACTTAGGTGAAGTCTTCATCGCTCAAAGCAAGGGACTTTAC - 2400
- A K L R S L N L G E V F I A Q S K G L Y
- Q S C D H S T * V K S S S L K A R D F T
- K V A I T Q L R * S L H R S K Q G T L P
2401 - CGTCAGTGATACGTGGCAAGGAGCAGCTGCAACTACTCATGCCTCTTAAGGCACCAAAA - 2460
- R Q C I R G K E Q L Q L L M P L K A P K
- V S V Y V A R S S C N Y S C L L R H Q K
- S V Y T W Q G A A A T T H A S * G T K R
2461 - GAAGTAACCTTTCTTGAAGGTGATTACATGACACAGTACTTACCTCTGAGGAGGTTGTT - 2520
- E V T F L E G D S H D T V L T S E E V V
- K * P F L K V I H M T Q Y L P L R R L F
- S N L S * R * F T * H S T Y L * G G C S
2521 - CTCAAGAACGGTGAACCTCGAAGCACTCGAGACGCCCGTTGATAGCTTCACAAATGGAGCT - 2580
- L K N G E L E A L E T P V D S F T N G A
- S R T V N S K H S R R P L I A S Q M E L
- Q E R * T R S T R D A R * * L H K W S Y
2581 - ATCGTTGGCACACAGTCTGTGTAAATGGCCTCATGCTCTTAGAGATTAAGGACAAAGAA - 2640
- I V G T P V C V N G L M L L E I K D K E
- S L A H Q S V * M A S C S * R L R T K N
- R W H T S L C K W P H A L R D * G Q R T
2641 - CAATACTGCGCATTGTCTCTGGTTTACTGGCTACAAACAATGTCTTTCGCTTAAAAGGG - 2700
- Q Y C A L S P G L L A T N N V F R L K G
- N T A H C L L V Y W L Q T M S F A * K G
- I L R I V S W F T G Y K Q C L S L K R G

FIG. 4 Cont'd

2701 - GGTGCACCAATTAAAGGTGTAACCTTTGGAGAAGATACTGTTTGGGAAGTTCAAGGTTAC - 2760
- G A P I K G V T F G E D T V W E V Q G Y
- V H Q L K V * P L E K I L F G K F K V T
- C T N * R C N L W R R Y C L G S S R L Q
2761 - AAGAATGTGAGAATCACATTTGAGCTTGATGAACGTGTTGACAAAGTGCTTAATGAAAAG - 2820
- K N V R I T F E L D E R V D K V L N E K
- R M * E S H L S L M N V L T K C L M K S
- E C E N H I * A * * T C * Q S A * * K V
2821 - TGCTCTGTCTACACTGTTGAATCCGGTACCGAAGTTACTGAGTTTGCATGTGTTGTAGCA - 2880
- C S V Y T V E S G T E V T E F A C V V A
- A L S T L L N P V P K L L S L H V L * Q
- L C L H C * I R Y R S Y * V C M C C S R
2881 - GAGGCTGTTGTGAAGACTTTACAACCAAGTTTCTGATCTCCTTACCAACATGGGTATTGAT - 2940
- E A V V K T L Q P V S D L L T N M G I D
- R L L * R L Y N Q F L I S L P T W V L I
- G C C E D F T T S F * S P Y Q H G Y * S
2941 - CTTGATGAGTGGAGTGTAGCTACATTCTACTTATTTGATGATGCTGGTGAAGAAAACTTT - 3000
- L D E W S V A T F Y L F D D A G E E N F
- L M S G V * L H S T Y L M M L V K K T F
- * * V E C S Y I L L I * * C W * R K L F
3001 - TCATCAGTATGTATTGTTCCCTTTTACCCTCCAGATGAGGAAGAAGAGGACGATGCAGAG - 3060
- S S R M Y C S F Y P P D E E E E D D A E
- H H V C I V P F T L Q M R K K R T M Q S
- I T Y V L F L L P S R * G R R G R C R V
3061 - TGTGAGGAAGAAGAAATTGATGAAACCTGTGAACATGAGTACGGTACAGAGGATGATTAT - 3120
- C E E E E I D E T C E H E Y G T E D D Y
- V R K K K L M K P V N M S T V Q R M I I
- * G R R N * * N L * T * V R Y R G * L S
3121 - CAAGGTCTCCCTCTGGAATTTGGTGCCTCAGCTGAAACAGTTCGAGTTGAGGAAGAAGAA - 3180
- Q G L P L E F G A S A E T V R V E E E E
- K V S L W N L V P Q L K Q F E L R K K K
- R S P S G I W C L S * N S S S * G R R R
3181 - GAGGAAGACTGGCTGGATGATACTACTGAGCAATCAGAGATTGAGCCAGAACCAGAACCT - 3240
- E E D W L D D T T E Q S E I E P E P E P
- R K T G W M I L L S N Q R L S Q N Q N L
- G R L A G * Y Y * A I R D * A R T R T Y
3241 - ACACCTGAAGAACCAGTTAATCAGTTTACTGGTTATTTAAACTTACTGACAATGTTGCC - 3300
- T P E E P V N Q F T G Y L K L T D N V A
- H L K N Q L I S L L V I * N L L T M L P
- T * R T S * S V Y W L F K T Y * Q C C H
3301 - ATTAAATGTGTTGACATCGTTAAGGAGGCACAAAGTGCTAATCCTATGGTGATTGTTAAAT - 3360
- I K C V D I V K E A Q S A N P M V I V N
- L N V L T S L R R H K V L I L W * L * M
- * M C * H R * G G T K C * S Y G D C K C
3361 - GCTGCTAACATACACCTGAAACATGGTGGTGGTAGCAGGTGCACTCAACAAGGCAACC - 3420
- A A N I H L K H G G G V A G A L N K A T
- L L T Y T * N M V V V * Q V H S T R Q P
- C * H T P E T W W W C S R C T Q Q G N Q
3421 - AATGGTGCCATGCAAAAAGGAGAGTGATGATTACATTAAAGCTAAATGGCCCTCTTACAGTA - 3480
- N G A M Q K E S D D Y I K L N G P L T V
- M V P C K R R V M I T L S * M A L L Q *
- W C H A K G E * * L H * A K W P S Y S R
3481 - GGAGGGTCTTGTGTTGCTTTCTGGACATAATCTTGCTAAGAAGTGCTGCATGTTGTTGGA - 3540
- G G S C L L S G H N L A K K C L H V V G
- E G L V C F L D I I L L R S V C M L L D
- R V L F A F W T * S C * E V S A C C W T
3541 - CCTAACCTAAATGCAGGTGAGGACATCCAGCTTCTTAAGGCAGCATATGAAAATTTCAT - 3600
- P N L N A G E D I Q L L K A A Y E N F N
- L T * M Q V R T S S F L R Q H M K I S I
- * P K C R * G H P A S * G S I * K F Q F

FIG. 4 Cont'd

3601 - TCACAGGACATCTTACTTGCACCATTGTTGTGTCAGCAGGCATATTTGGTGCTAAACCACTT - 3660
- S Q D I L L A P L L S A G I F G A K P L
- H R T S Y L H H C C Q Q A Y L V L N H F
- T G H L T C T I V V S R H I W C * T T S
3661 - CAGTCTTTACAAGTGTGCGTGCAGACGGTTCGTACACAGGTTTATATTGCAGTCAATGAC - 3720
- Q S L Q V C V Q T V R T Q V Y I A V N D
- S L Y K C A C R R F V H R F I L Q S M T
- V F T S V R A D G S Y T G L Y C S Q * Q
3721 - AAAGCTCTTTATGAGCAGGTTGTCATGGATTATCTTGATAACCTGAAGCCTAGAGTGGAA - 3780
- K A L Y E Q V V M D Y L D N L K P R V E
- K L F M S R L S W I I L I T * S L E W K
- S S L * A G C H G L S * * P E A * S G S
3781 - GCACCTAAACAAGAGGCCACCAACAGAAGATTCCAAAACCTGAGGAGAAATCTGTC - 3840
- A P K Q E E P P N T E D S K T E E K S V
- H L N K R S H Q T Q K I P K L R R N L S
- T * T R G A T K H R R F Q N * G E I C R
3841 - GTACAGAAGCCTGTCGATGTGAAGCCAAAATTAAGGCCTGCATTGATGAGGTTACCACA - 3900
- V Q K P V D V K P K I K A C I D E V T T
- Y R S L S M * S Q K L R P A L M R L P Q
- T E A C R C E A K N * G L H * * G Y H N
3901 - ACACCTGGAAGAACTAAGTTTCTTACCAATAAGTTACTCTTGTGCTGATATCAATGGT - 3960
- T L E E T K F L T N K L L L F A D I N G
- H W K K L S F L P I S Y S C L L I S M V
- T G R N * V S Y Q * V T L V C * Y Q W *
3961 - AAGCTTTACCATGATTCTCAGAACATGCTTAGAGGTGAAGATATGCTTTCTTGGAGAAG - 4020
- K L Y H D S Q N M L R G E D M S F L E K
- S F T M I L R T C L E V K I C L S L R R
- A L P * F S E H A * R * R Y V F P * E G
4021 - GATGCACCTTACATGGTAGGTGATGTTACTAGTGGTGATATCACTTGTGTTGTAATA - 4080
- D A P Y M V G D V I T S G D I T C V V I
- M H L T W * V M L S L V V I S L V L * Y
- C T L H G R * C Y H * W * Y H L C C N T
4081 - CCCTCCAAAAGGCTGGTGGCACTACTGAGATGCTCTCAAGAGCTTTGAAGAAAGTGCCA - 4140
- P S K K A G G T T E M L S R A L K K V P
- P P K R L V A L L R C S Q E L * R K C Q
- L Q K G W W H Y * D A L K S F E E S A S
4141 - GTTGAGTATATAACCACGTACCCTGGACAAGGATGTGCTGGTTATACACTTGAGGAA - 4200
- V D E Y I T T Y P G Q G C A G Y T L E E
- L M S I * P R T L D K D V L V I H L R K
- * * V Y N H V P W T R M C W L Y T * G S
4201 - GCTAAGACTGCTCTTAAGAAATGCAATCTGCATTTTATGTACTACCTTCAGAAGCACCT - 4260
- A K T A L K K C K S A F Y V L P S E A P
- L R L L L R N A N L H F M Y Y L Q K H L
- * D C S * E M Q I C I L C T T F R S T *
4261 - AATGCTAAGGAAGAGATTCTAGGAACGTATCCTGGAATTTGAGAGAAATGCTTGCTCAT - 4320
- N A K E E I L G T V S W N L R E M L A H
- M L R K R F * E L Y P G I * E K C L L M
- C * G R D S R N C I L E F E R N A C S C
4321 - GCTGAAGAGACAAGAAAATTAATGCCTATATGCATGGATGTTAGAGCCATAATGGCAACC - 4380
- A E E T R K L M P I C M D V R A I M A T
- L K R Q E N * C L Y A W M L E P * W Q P
- * R D K K I N A Y M H G C * S H N G N H
4381 - ATCCAACGTAAGTATAAAGGAATTAATAATCAAGAGGGCATCGTTGACTATGGTGTCGGA - 4440
- I Q R K Y K G I K I Q E G I V D Y G V R
- S N V S I K E L K F K R A S L T M V S D
- P T * V * R N * N S R G H R * L W C P I
4441 - TTCTTCTTTTATACTAGTAAAGAGCCTGTAGCTTCTATTATTACGAAGCTGAACCTCTTA - 4500
- F F F Y T S K E P V A S I I T K L N S L
- S S F I L V K S L * L L L L R S * T L *
- L L L Y * * R A C S F Y Y Y E A E L S K

FIG. 4 Cont'd

4501 - AATGAGCCGCTTGTCACAATGCCAATTGGTTATGTGACACATGGTTTTAATCTTGAAGAG - 4560
- N E P L V T M P I G Y V T H G F N L E E
- M S R L S Q C Q L V M * H M V L I L K R
- * A A C H N A N W L C D T W F * S * R G
4561 - GCTGCGCGCTGATGCGTTCTCTTAAAGCTCCTGCCGTAGTGTGAGTATCATCACCAGAT - 4620
- A A R C M R S L K A P A V V S V S S P D
- L R A V C V L L K L L P * C Q Y H H Q M
- C A L Y A F S * S S C R S V S I I T R C
4621 - GCTGTTACTACATATAATGGATACCTCACTTCGTCATCAAAGACATCTGAGGAGCACTTT - 4680
- A V T T Y N G Y L T S S S K T S E E H F
- L L L H I M D T S L R H Q R H L R S T L
- C Y Y I * W I P H F V I K D I * G A L C
4681 - GTAGAAACAGTTTCTTTGGCTGGCTTACAGAGATTGGTCTTATTCAGGACAGCGTACA - 4740
- V E T V S L A G S Y R D W S Y S G Q R T
- * K Q F L W L A L T E I G P I Q D S V Q
- R N S F F G W L L Q R L V L F R T A Y R
4741 - GAGTTAGGTGTGAATTTCTTAAGCGTGGTGACAAAATTGTGTACCACACTCTGGAGAGC - 4800
- E L G V E F L K R G D K I V Y H T L E S
- S * V L N F L S V V T K L C T T L W R A
- V R C * I S * A W * Q N C V P H S G E P
4801 - CCCGTCGAGTTTCATCTTGACGGTGAGTTCTTCACTTGACAACTAAAGAGTCTCTTA - 4860
- P V E F H L D G E V L S L D K L K S L L
- P S S F I L T V R F F H L T N * R V S Y
- R R V S S * R * G S F T * Q T K E S L I
4861 - TCCCTGCGGGAGGTTAAGACTATAAAAGTGTTCACAACTGTGGACAACACTAATCTCCAC - 4920
- S L R E V K T I K V F T T V D N T N L H
- P C G R L R L * K C S Q L W T T L I S T
- P A G G * D Y K S V H N C G Q H * S P H
4921 - ACACAGCTTGTGGATATGTCTATGACATATGGACAGCAGTTTGGTCCAACATACTTGGAT - 4980
- T Q L V D M S M T Y G Q Q F G P T Y L D
- H S L W I C L * H M D S S L V Q H T W M
- T A C G Y V Y D I W T A V W S N I L G W
4981 - GGTGCTGATGTTACAAAAATTAACTCATGTAATCATGAGGGTAAGACTTTCTTTGTA - 5040
- G A D V T K I K P H V N H E G K T F F V
- V L M L Q K L N L M * I M R V R L S L Y
- C * C Y K N * T S C K S * G * D F L C T
5041 - CTACCTAGTGATGACACACTACGTAGTGAAGCTTTCGAGTACTACCATACTCTTGATGAG - 5100
- L P S D D T L R S E A F E Y Y H T L D E
- Y L V M T H Y V V K L S S T T I L L M R
- T * * * H T T * * S F R V L P Y S * * E
5101 - AGTTTTCTTGGTAGGTACATGTCTGCTTTAAACCACACAAAGAAATGGAAATTTCTCAA - 5160
- S F L G R Y M S A L N H T K K W K F P Q
- V F L V G T C L L * T T Q R N G N F L K
- F S W * V H V C F K P H K E M E I S S S
5161 - GTTGGTGGTTAACTTCAATTAATGGGCTGATAACAATTGTTATTTGTCTAGTGTTTTA - 5220
- V G G L T S I K W A D N N C Y L S S V L
- L V V * L Q L N G L I T I V I C L V F Y
- W W F N F N * M G * * Q L L F V * C F I
5221 - TTAGCACTTCAACAGCTTGAAGTCAAATTCATGCACCAGCACTTCAAGAGGCTTATTAT - 5280
- L A L Q Q L E V K F N A P A L Q E A Y Y
- * H F N S L K S N S M H Q H F K R L I I
- S T S T A * S Q I Q C T S T S R G L L *
5281 - AGAGCCCGTGCTGGTGATGCTGCTAACTTTTGTGCACTCATACTCGCTTACAGTAATAAA - 5340
- R A R A G D A A N F C A L I L A Y S N K
- E P V L V M L L T F V H S Y S L T V I K
- S P C W * C C * L L C T H T R L Q * * N
5341 - ACTGTTGGCGAGCTTGGTGATGTGAGAGAACTATGACCCATCTTCTACAGCATGCTAAT - 5400
- T V G E L G D V R E T M T H L L Q H A N
- L L A S L V M S E K L * P I F Y S M L I
- C W R A W * C Q R N Y D P S S T A C * F

FIG. 4 Cont'd

5401 - TTGGAATCTGCAAAGCGAGTTCTTAATGTGGTGTGTAAACATTGTGGTCAGAAAACACTACT - 5460
- L E S A K R V L N V V C K H C G Q K T T
- W N L Q S E F L M W C V N I V V R K L L
- G I C K A S S * C G V * T L W S E N Y Y
5461 - ACCTTAACGGGTGTAGAAGCTGTGATGTATATGGGTACTCTATCTTATGATAATCTTAAG - 5520
- T L T G V E A V M Y M G T L S Y D N L K
- P * R V * K L * C I W V L Y L M I I L R
- L N G C R S C D V Y G Y S I L * * S * D
5521 - ACAGGTGTTTCCATTCCATGTGTGTGTGGTCGTGATGCTACACAATATCTAGTACAACAA - 5580
- T G V S I P C V C G R D A T Q Y L V Q Q
- Q V F P F H V C V V V M L H N I * Y N K
- R C F H S M C V W S * C Y T I S S T T R
5581 - GAGTCTTCTTTTGTATGATGTCTGCACCACCTGTGAGTATAAATTACAGCAAGGTACA - 5640
- E S S F V M M S A P P A E Y K L Q Q G T
- S L L L L * C L H H L L S I N Y S K V H
- V F F C Y D V C T T C * V * I T A R Y I
5641 - TTCTTATGTGCGAATGAGTACACTGGTAACTATCAGTGTGGTCATTACACTCATATAACT - 5700
- F L C A N E Y T G N Y Q C G H Y T H I T
- S Y V R M S T L V T I S V V I T L I * L
- L M C E * V H W * L S V W S L H S Y N C
5701 - GCTAAGGAGACCCTCTATCGTATTGACGGAGCTCACCTTACAAAGATGCAGAGTACAAA - 5760
- A K E T L Y R I D G A H L T K M S E Y K
- L R R P S I V L T E L T L Q R C Q S T K
- * G D P L S Y * R S S P Y K D V R V Q R
5761 - GGACCAGTGACTGATGTTTCTACAAGGAAACATCTTACACTACAACCATCAAGCCTGTG - 5820
- G P V T D V F Y K E T S Y T T T I K P V
- D Q * L M F S T R K H L T L Q P S S L C
- T S D * C F L Q G N I L H Y N H Q A C V
5821 - TCGTATAAACTCGATGGAGTTACTTACACAGAGATTGAACCAAATTTGGATGGGTATTAT - 5880
- S Y K L D G V T Y T E I E P K L D G Y Y
- R I N S M E L L T Q R L N Q N W M G I I
- V * T R W S Y L H R D * T K I G W V L *
5881 - AAAAAGGATAATGCTTACTATACAGAGCAGCCTATAGACCTTGTACCAACTCAACCATTA - 5940
- K K D N A Y Y T E Q P I D L V P T Q P L
- K R I M L T I Q S S L * T L Y Q L N H Y
- K G * C L L Y R A A Y R P C T N S T I T
5941 - CCAAATGCGAGTTTGTATAATTTCAAACCTCACATGTTCTAACACAAAATTTGCTGATGAT - 6000
- P N A S F D N F K L T C S N T K F A D D
- Q M R V L I I S N S H V L T Q N L L M I
- K C E F * * F Q T H M F * H K I C * * F
6001 - TTAATCAAATGACAGGCTTCACAAAGCCAGCTTCACGAGAGCTATCTGTACATTCTTC - 6060
- L N Q M T G F T K P A S R E L S V T F F
- * I K * Q A S Q S Q L H E S Y L S H S S
- K S N D R L H K A S F T R A I C H I L P
6061 - CCAGACTTGAATGGCGATGTAGTGGCTATTGACTATAGACACTATTACAGCGAGTTTCAAG - 6120
- P D L N G D V V A I D Y R H Y S A S F K
- Q T * M A M * W L L T I D T I Q R V S R
- R L E W R C S G Y * L * T L F S E F Q E
6121 - AAAGGTGCTAAATTACTGCATAAGCCAATTGTTTGGCACATTAACCAGGCTACAACCAAG - 6180
- K G A K L L H K P I V W H I N Q A T T K
- K V L N Y C I S Q L F G T L T R L Q P R
- R C * I T A * A N C L A H * P G Y N Q D
6181 - ACAACGTTCAAACCAAACACTTGGTGTTTACGTTGTCTTTGGAGTACAAAGCCAGTAGAT - 6240
- T T F K P N T W C L R C L W S T K P V D
- Q R S N Q T L G V Y V V F G V Q S Q * I
- N V Q T K H L V F T L S L E Y K A S R Y
6241 - ACTTCAAATTCATTGAAGTTCTGGCAGTAGAAGACACACAAGGAATGGACAATCTTGCT - 6300
- T S N S F E V L A V E D T Q G M D N L A
- L Q I H L K F W Q * K T H K E W T I L L
- F K F I * S S G S R R H T R N G Q S C L

FIG. 4 Cont'd

6301 - TGTGAAAGTCAACAACCCACCTCTGAAGAAGTAGTGGAAAATCCTACCATACAGAAGGAA - 6360
- C E S Q Q P T S E E V V E N P T I Q K E
- V K V N N P P L K K * W K I L P Y R R K
- * K S T T H L * R S S G K S Y H T E G S
6361 - GTCATAGAGTGTGACGTGAAAACCTACCGAAGTTGTAGGCAATGTCATACTTAAACCATCA - 6420
- V I E C D V K T T E V V G N V I L K P S
- S * S V T * K L P K L * A M S Y L N H Q
- H R V * R E N Y R S C R Q C H T * T I R
6421 - GATGAAGGTGTTAAAGTAACACAAGAGTTAGGTCATGAGGATCTTATGGCTGCTTATGTG - 6480
- D E G V K V T Q E L G H E D L M A A Y V
- M K V L K * H K S * V M R I L W L L M W
- * R C * S N T R V R S * G S Y G C L C G
6481 - GAAAACACAAGCATTACCATTAAGAAACCTAATGAGCTTCACTAGCCTTAGGTTTAAAA - 6540
- E N T S I T I K K P N E L S L A L G L K
- K T Q A L P L R N L M S F H * P * V * K
- K H K H Y H * E T * * A F T S L R F K N
6541 - ACAATTGCCACTCATGGTATTGCTGCAATTAATAGTGTTCCTGGAGTAAAATTTGGCT - 6600
- T I A T H G I A A I N S V P W S K I L A
- Q L P L M V L L Q L I V F L G V K F W L
- N C H S W Y C C N * * C S L E * N F G L
6601 - TATGTCAAACCATTCTTAGGACAAGCAGCAATTACAACATCAAATTGCGCTAAGAGATTA - 6660
- Y V K P F L G Q A A I T T S N C A K R L
- M S N H S * D K Q Q L Q H Q I A L R D *
- C Q T I L R T S S N Y N I K L R * E I S
6661 - GCACAACGTGTGTTTAAACAATTATATGCCTTATGTGTTTACATTATTGTTCCAATTGTGT - 6720
- A Q R V F N N Y M P Y V F T L L F Q L C
- H N V C L T I I C L M C L H Y C S N C V
- T T C V * Q L Y A L C V Y I I V P I V Y
6721 - ACTTTTACTAAAAGTACCAATCTAGAAATAGAGCTTCACTACCTACAACCTATTGCTAAA - 6780
- T F T K S T N S R I R A S L P T T I A K
- L L L K V P I L E L E L H Y L Q L L L K
- F Y * K Y Q F * N * S F T T Y N Y C * K
6781 - AATAGTGTAAAGAGTGTGCTAAATTATGTTGGATGCCGCATTAATTATGTGAAGTCA - 6840
- N S V K S V A K L C L D A G I N Y V K S
- I V L R V L L N Y V W M P A L I M * S H
- * C * E C C * I M F G C R H * L C E V T
6841 - CCCAAATTTTCTAAATTGTTTACAATCGCTATGTGGCTATTGTTGTTAAGTATTTGCTTA - 6900
- P K F S K L F T I A M W L L L L S I C L
- P N F L N C S Q S L C G Y C C * V F A *
- Q I F * I V H N R Y V A I V V K Y L R
6901 - GGTTCTCTAATCTGTGTAACGTGCTTTTGGTGTACTCTTATCTAATTTTGGTGCTCCT - 6960
- G S L I C V T A A F G V L L S N F G A P
- V L * S V * L L L L V Y S Y L I L V L L
- F S N L C N C C F W C T L I * F W C S F
6961 - TCTTATTGTAATGGCGTTAGAGAATTGTATCTTAATTCGTCTAACGTTACTACTATGGAT - 7020
- S Y C N G V R E L Y L N S S N V T T M D
- L I V M A L E N C I L I R L T L L L W I
- L L * W R * R I V S * F V * R Y Y Y G F
7021 - TTCTGTGAAGGTTCTTTTCCTTGCAGCATTTGTTTAAAGTGGATTAGACTCCCTTGATTCT - 7080
- F C E G S F P C S I C L S G L D S L D S
- S V K V L F L A A F V * V D * T P L I L
- L * R F F S L Q H L F K W I R L P * F L
7081 - TATCCAGCTCTTGAAACCATTGAGGTGACGATTTTCATCGTACAAGCTAGACTTGACAATT - 7140
- Y P A L E T I Q V T I S S Y K L D L T I
- I Q L L K P F R * R F H R T S * T * Q F
- S S S * N H S G D D F I V Q A R L D N F
7141 - TTAGGTCTGGCCGCTGAGTGGGTTTTGGCATATATGTTGTTTACAAAATTCTTTTATTA - 7200
- L G L A A E W V L A Y M L F T K F F Y L
- * V W P L S G F W H I C C S Q N S F I Y
- R S G R * V G F G I Y V V H K I L L F I

FIG. 4 Cont'd

7201 - TTAGGTCTTTCAGCTATAATGCAGGTGTTCTTTGGCTATTTTGCTAGTCATTTTCATCAGC - 7260
- L G L S A I M Q V F F G Y F A S H F I S
- * V F Q L * C R C S L A I L L V I S S A
- R S F S Y N A G V L W L F C * S F H Q Q
7261 - AATTCTTGGCTCATGTGGTTTATCATTAGTATTGTACAAATGGCACCCGTTTCTGCAATG - 7320
- N S W L M W F I I S I V Q M A P V S A M
- I L G S C G L S L V L Y K W H P F L Q W
- F L A H V V Y H * Y C T N G T R F C N G
7321 - GTTAGGATGTACATCTTCTTTGCTTCTTTCTACTACATATGGAAGAGCTATGTTTCATATC - 7380
- V R M Y I F F A S F Y Y I W K S Y V H I
- L G C T S S L L L S T T Y G R A M F I S
- * D V H L L C F F L L H M E E L C S Y H
7381 - ATGGATGGTGCACCTCTTCGACTTGCATGATGTGCTATAAGCGCAATCGTGCCACACGC - 7440
- M D G C T S S T C M M C Y K R N R A T R
- W M V A P L R L A * C A I S A I V P H A
- G W L H L F D L H D V L * A Q S C H T R
7441 - GTTGAGTGTACAACCTATTGTTAATGGCATGAAGAGATCTTTCTATGTCTATGCAAATGGA - 7500
- V E C T T I V N G M K R S F Y V Y A N G
- L S V Q L L L M A * R D L S M S M Q M E
- * V Y N Y C * W H E E I F L C L C K W R
7501 - GGCCGTGGCTTCTGCAAGACTCACAATTGGAATTGTCTCAATTGTGACACATTTTGCAC - 7560
- G R G F C K T H N W N C L N C D T F C T
- A V A S A R L T I G I V S I V T H F A L
- P W L L Q D S Q L E L S Q L * H I L H W
7561 - GGTAGTACATTCATTAGTGATGAAGTTGCTCGTATTTGTCACTCCAGTTTAAAGACCA - 7620
- G S T F I S D E V A R D L S L Q F K R P
- V V H S L V M K L L V I C H S S L K D Q
- * Y I H * * * S C S * F V T P V * K T N
7621 - ATCAACCTACTGACCAGTCATCGTATATTGTTGATAGTGTGCTGTGAAAAATGGCGCG - 7680
- I N P T D Q S S Y I V D S V A V K N G A
- S T L L T S H R I L L I V L L * K M A R
- Q P Y * P V I V Y C * * C C C E K W R A
7681 - CTTACCTCTACTTTGACAAGGCTGGTCAAAAGACCTATGAGAGACATCCTCTCTCCCAT - 7740
- L H L Y F D K A G Q K T Y E R H P L S H
- F T S T L T R L V K R P M R D I L S P I
- S P L L * Q G W S K D L * E T S S L P F
7741 - TTTGTCAATTTAGACAATTTGAGAGCTAACAACACTAAAGGTTCACTGCCTATTAATGTC - 7800
- F V N L D N L R A N N T K G S L P I N V
- L S I * T I * E L T T L K V H C L L M S
- C Q F R Q F E S * Q H * R F T A Y * C H
7801 - ATAGTTTTTGATGGCAAGTCCAAATGCGACGAGTCTGCTTCTAAGTCTGCTTCTGTGTAC - 7860
- I V F D G K S K C D E S A S K S A S V Y
- * F F L M A S P N A T S L L L S L L L C T
- S F * W Q V Q M R R V C F * V C F C V L
7861 - TACAGTCAGCTGATGTGCCAACCTATTCTGTTGCTTGACCAAGCTCTTGATCAGACGTT - 7920
- Y S Q L M C Q P I L L L D Q A L V S D V
- T V S * C A N L F C C L T K L L Y Q T L
- Q S A D V P T Y S V A * P S S C I R R W
7921 - GGAGATAGTACTGAAGTTTCCGTTAAGATGTTTGATGCTTATGTGACACCTTTTCAGCA - 7980
- G D S T E V S V K M F D A Y V D T F S A
- E I V L K F P L R C L M L M S T P F Q Q
- R * Y * S F R * D V * C L C R H L F S N
7981 - ACTTTTAGTGTTCCTATGGAAAACTTAAGGCACTTGTGCTACAGCTCACAGCGAGTTA - 8040
- T F S V P M E K L K A L V A T A H S E L
- L L V F L W K N L R H L L L Q L T A S *
- F * C S Y G K T * G T C C Y S S Q R V S
8041 - GCAAAGGGGTAGCTTTAGATGGTGTCTTTCTACATTCGTGTGCTGAGCTGCCCGACAAGGT - 8100
- A K G V A L D G V L S T F V S A A R Q G
- Q R V * L * M V S F L H S C Q L P D K V
- K G C S F R W C P F Y I R V S C P T R C

FIG. 4 Cont'd

8101 - GTTGTGATACCGATGTTGACACAAAGGATGTTATTGAATGTCTCAAACTTTCACATCAC - 8160
- V V D T D V D T K D V I E C L K L S H H
- L L I P M L T Q R M L L N V S N F H I T
- C * Y R C * H K G C Y * M S Q T F T S L
8161 - TCTGACTTAGAAGTGACAGGTGACAGTTGTAACAATTCATGCTCACCTATAATAAGGTT - 8220
- S D L E V T G D S C N N F M L T Y N K V
- L T * K * Q V T V V T I S C S P I I R L
- * L R S D R * Q L * Q F H A H L * * G *
8221 - GAAAACATGACGCCAGAGATCTTGGCGCATGTATTGACTGTAATGCAAGGCATATCAAT - 8280
- E N M T P R D L G A C I D C N A R H I N
- K T * R P E I L A H V L T V M Q G I S M
- K H D A Q R S W R M Y * L * C K A Y Q C
8281 - GCCCAAGTAGCAAAAAGTCACAATGTTTCACTCATCTGGAATGTAAAAGACTACATGTCT - 8340
- A Q V A K S H N V S L I W N V K D Y M S
- P K * Q K V T M F H S S G M * K T T C L
- P S S K K S Q C F T H L E C K R L H V F
8341 - TTATCTGAACAGCTGCGTAAACAAATTCGTAGTCTGCCAAGAAGAACAACATACCTTTT - 8400
- L S E Q L R K Q I R S A A K K N N I P F
- Y L N S C V N K F V V L P R R T T Y L L
- I * T A A * T N S * C C Q E E Q H T F *
8401 - AGACTAAGTGTGCTACAAGTACAGGTTGTCAATGTCATAACTACTAAAATCTCACTC - 8460
- R L T C A T T R Q V V N V I T T K I S L
- D * L V L Q L D R L S M S * L L K S H S
- T N L C Y N * T G C Q C H N Y * N L T Q
8461 - AAGGGTGGTAAGATTGTTAGTACTTGTTTTAAACTTATGCTTAAGGCCACATTATTGTGC - 8520
- K G G K I V S T C F K L M L K A T L L C
- R V V R L L V L V L N L C L R P H Y C A
- G W * D C * Y L F * T Y A * G H I I V R
8521 - GTTCTTGCTGCATTGGTTTGTATATCGTTATGCCAGTACATACATTGTCAATCCATGAT - 8580
- V L A A L V C Y I V M P V H T L S I H D
- F L L H W F V I S L C Q Y I H C Q S M M
- S C C I G L L Y R Y A S T Y I V N P * W
8581 - GGTTACACAAATGAAATCATTGGTTACAAAGCCATTGAGGATGGTGTCACTCGTGACATC - 8640
- G Y T N E I I G Y K A I Q D G V T R D I
- V T Q M K S L V T K P F R M V S L V T S
- L H K * N H W L Q S H S G W C H S * H H
8641 - ATTTCTACTGATGATTGTTTTGCAAATAAACATGCTGGTTTTGACGCATGGTTTAGCCAG - 8700
- I S T D D C F A N K H A G F D A W F S Q
- F L L M I V L Q I N M L V L T H G L A S
- F Y * * L F C K * T C W F * R M V * P A
8701 - CGTGGTGGTTTCATACAAAATGACAAAAGCTGCCCTGTAGTAGCTGCTATCATTACAAGA - 8760
- R G G S Y K N D K S C P V V A A I I T R
- V V V H T K M T K A A L * * L L S L Q E
- W W F I Q K * Q K L P C S S C Y H Y K R
8761 - GAGATTGGTTTCATAGTGCCTGGCTTACGGGTACTGTGCTGAGAGCAATCAATGGTGAC - 8820
- E I G F I V P G L P G T V L R A I N G D
- R L V S * C L A Y R V L C * E Q S M V T
- D W F H S A W L T G Y C A E S N Q W * L
8821 - TTCTTGCAATTTCTACCTCGTGTTTTGTAGTGTGTTGGCAACATTGCTACACACCTTCC - 8880
- F L H F L P R V F S A V G N I C Y T P S
- S C I F Y L V F L V L L A T F A T H L P
- L A F S T S C F * C C W Q H L L H T F Q
8881 - AAACCTATTGAGTATAGTATTGCTACCTCTGCTTGGCTTCTTGCTGCTGAGTGTACA - 8940
- K L I E Y S D F A T S A C V L A A E C T
- N S L S I V I L L P L L A F L L L S V Q
- T H * V * * F C Y L C L R S C C * V Y N
8941 - ATTTTAAAGGATGCTATGGGCAAACCTGTGCCATATTGTTATGACACTAATTGCTAGAG - 9000
- I F K D A M G K P V P Y C Y D T N L L E
- F L R M L W A N L C H I V M T L I C * R
- F * G C Y G Q T C A I L L * H * F A R G

FIG. 4 Cont'd

9001 - GGTTCATTTCTTATAGTGAGCTTCGTCAGACACTCGTTATGTGCTTATGGATGGTTCC - 9060
- G S I S Y S E L R P D T R Y V L M D G S
- V L F L I V S F V Q T L V M C L W M V P
- F Y F L * * A S S R H S L C A Y G W F H
9061 - ATCATACAGTTTCCTAACACTTACCTGGAGGGTCTGTTAGAGTAGTAACAACCTTTTGAT - 9120
- I I Q F P N T Y L E G S V R V V T T F D
- S Y S F L T L T W R V L L E * * Q L L M
- H T V S * H L P G G F C * S S N N F * C
9121 - GCTGAGTACTGTAGACATGGTACATGCGAAAGGTCAGAAGTAGGTATTTGCCTATCTACC - 9180
- A E Y C R H G T C E R S E V G I C L S T
- L S T V D M V H A K G Q K * V F A Y L P
- * V L * T W Y M R K V R S R Y L P I Y Q
9181 - AGTGGTAGATGGGTTCTTAATAATGAGCATTACAGAGCTCTATCAGGAGTTTTCTGTGGT - 9240
- S G R W V L N N E H Y R A L S G V F C G
- V V D G F L I M S I T E L Y Q E F S V V
- W * M G S * * * A L Q S S I R S F L W C
9241 - GTTGATGCGATGAATCTCATAGCTAACATCTTTACTCCTCTGTGCAACCTGTGGGTGCT - 9300
- V D A M N L I A N I F T P L V Q P V G A
- L M R * I S * L T S L L L L C N L W V L
- * C D E S H S * H L Y S S C A T C G C F
9301 - TTAGATGTGTCTGCTTCAGTAGTGGTGGTATTATTGCCATATTGGTGAAGTGTGCT - 9360
- L D V S A S V V A G G I I A I L V T C A
- * M C L L Q * W L V V L L P Y W * L V L
- R C V C F S S G W W Y Y C H I G D L C C
9361 - GCCTACTACTTTATGAAATTCAGACGTGCTTTTGGTGAGTACAACCATGTTGTTGCTGCT - 9420
- A Y Y F M K F R R A F G E Y N H V V A A
- P T T L * N S D V L L V S T T M L L L L
- L L L Y E I Q T C F W * V Q P C C C C *
9421 - AATGCACTTTTGTGTTTGTGCTTTTACTACTCTGTCTGGCACCAGCTTACAGCTTT - 9480
- N A L L F L M S F T I L C L A P A Y S F
- M H F C F * C L S L Y S V W H Q L T A F
- C T F V F D V F H Y T L S G T S L Q L S
9481 - CTGCCGGGAGTCTACTCAGTCTTTTACTTGTACTTGACATTCTATTTACCAATGATGTT - 9540
- L P G V Y S V F Y L Y L T F Y F T N D V
- C R E S T Q S F T C T * H S I S P M M F
- A G S L L S L L L V L D I L F H Q * C F
9541 - TCATTCTTGGCTCACCTTCAATGGTTTGGCATGTTTCTCCTATTGTGCCTTTTGGATA - 9600
- S F L A H L Q W F A M F S P I V P F W I
- H S W L T F N G L P C F L L L C L F G *
- I L G S P S M V C H V F S Y C A F L D N
9601 - ACAGCAATCTATGTATTCTGTATTTCTCTGAAGCACTGCCATTGGTTCTTTAACAACAT - 9660
- T A I Y V F C I S L K H C H W F F N N Y
- Q Q S M Y S V F L * S T A I G S L T T I
- S N L C I L Y F S E A L P L V L * Q L S
9661 - CTTAGGAAAAGAGTCATGTTTAAATGGAGTTACATTTAGTACCTTCGAGGAGGCTGCTTTG - 9720
- L R K R V M F N G V T F S T F E E A A L
- L G K E S C L M E L H L V P S R R L L C
- * E K S H V * W S Y I * Y L R G G C F V
9721 - TGTACCTTTTTGCTCAACAAGGAAATGTACCTAAAATTGCGTAGCGAGACACTGTTGCCA - 9780
- C T F L L N K E M Y L K L R S E T L L P
- V P F C S T R K C T * N C V A R H C C H
- Y L F A Q Q G N V P K I A * R D T V A T
9781 - CTTACACAGTATAACAGGTATCTTGCTCTATATAACAAGTACAAGTATTTAGTGGAGCC - 9840
- L T Q Y N R Y L A L Y N K Y K Y F S G A
- L H S I T G I L Y I T S T S I S V E P
- Y T V * Q V S C S I * Q V Q V F Q W S L
9841 - TTAGATACTACCAGCTATCGTGAAGCAGCTTGCTGCCACTTAGCAAAGGCTCTAAATGAC - 9900
- L D T T S Y R E A A C C H L A K A L N D
- * I L P A I V K Q L A A T * Q R L * M T
- R Y Y Q L S * S S L L P L S K G S K * L

FIG. 4 Cont'd

9901 - TTTAGCAACTCAGGTGCTGATGTTCTCTACCAACCACCACAGACATCAATCACTTCTGCT - 9960
- F S N S G A D V L Y Q P P Q T S I T S A
- L A T Q V L M F S T N H H R H Q S L L L
- * Q L R C * C S L P T T T D I N H F C C
9961 - GTTCTGCAGAGTGTTTGTAGGAAAATGGCATTCCCGTCAGGCAAAGTTGAAGGGTGCATG - 10020
- V L Q S G F R K M A F P S G K V E G C M
- F C R V V L G K W H S R Q A K L K G A W
- S A E W F * E N G I P V R Q S * R V H G
10021 - GTACAAGTAACCTGTGGAACATACTCTTAATGGATTGTGGTTGGATGACACAGTATAC - 10080
- V Q V T C G T T T L N G L W L D D T V Y
- Y K * P V E L Q L L M D C G W M T Q Y T
- T S N L W N Y N S * W I V V G * H S I L
10081 - TGCCAAGACATGTCATTGTCACAGCAGAAGACATGCTTAATCCTAATATGAAGATCTG - 10140
- C P R H V I C T A E D M L N P N Y E D L
- V Q D M S F A Q Q K T C L I L T M K I C
- S K T C H L H S R R H A * S * L * R S A
10141 - CTCATTGCGAAATCCAACCATAGCTTTCTGTTTCAGGCTGGCAATGTTCAACTTCGTGTT - 10200
- L I R K S N H S F L V Q A G N V Q L R V
- S F A N P T I A F L F R L A M F N F V L
- H S Q I Q P * L S C S G W Q C S T S C Y
10201 - ATTGGCCATTCTATGCAAAATGTCTGCTTAGGCTTAAAGTTGATACTTCTAACCCTAAG - 10260
- I G H S M Q N C L L R L K V D T S N P K
- L A I L C K I V C L G L K L I L L T L R
- W P F Y A K L S A * A * S * Y F * P * D
10261 - ACACCCAAGTATAAATTTGTCCGTATCCAACCTGGTCAAACATTTTCAGTTCTAGCATGC - 10320
- T P K Y K F V R I Q P G Q T F S V L A C
- H P S I N L S V S N L V K H F Q F * H A
- T Q V * I C P Y P T W S N I F S S S M L
10321 - TACAATGGTTCACCATCTGGTGTATATCAGTGTGCCATGAGACCTAATCATACCATTAAA - 10380
- Y N G S P S G V Y Q C A M R P N H T I K
- T M V H H L V F I S V P * D L I I P L K
- Q W F T I W C L S V C H E T * S Y H * R
10381 - GGTCTTTCTCTAATGGATCATGTGGTAGTGTGGTTTAAACATTGATTATGATTGCGTG - 10440
- G S F L N G S C G S V G F N I D Y D C V
- V L S L M D H V V V L V L T L I M I A C
- F F P * W I M W * C W F * H * L * L R V
10441 - TCTTTCTGCTATATGCATCATATGGAGCTTCCAACAGGAGTACACGCTGGTACTGACTTA - 10500
- S F C Y M H H M E L P T G V H A G T D L
- L S A I C I I W S F Q Q E Y T L V L T *
- F L L Y A S Y G A S N R S T R W Y * L R
10501 - GAAGGTAAATCTATGGTCCATTGTTGACAGACAAACTGCACAGGCTGCAGGTACAGAC - 10560
- E G K F Y G P F V D R Q T A Q A A G T D
- K V N S M V H L L T D K L H R L Q V Q T
- R * I L W S I C * Q T N C T G C R Y R H
10561 - ACAACCATAACATTAAATGTTTTGGCATGGCTGTATGCTGCTGTTATCAATGGTGATAGG - 10620
- T T I T L N V L A W L Y A A V I N G D R
- Q P * H * M F W H G C M L L L S M V I G
- N H N I K C F G M A V C C C Y Q W * * V
10621 - TGGTTTCTTAATAGATTCACTACTTTGAATGACTTTAACCTTGTGGCAATGAAGTAC - 10680
- W F L N R F T T T L N D F N L V A M K Y
- G F L I D S P L L * M T L T L W Q * S T
- V S * * I H H Y F E * L * P C G N E V Q
10681 - AACTATGAACCTTTGACACAAGATCATGTTGACATATTGGGACCTCTTCTGCTCAAACA - 10740
- N Y E P L T Q D H V D I L G P L S A Q T
- T M N L * H K I M L T Y W D L F L L K Q
- L * T F D T R S C * H I G T S F C S N R
10741 - GGAATTGCCGTCTTAGATATGTGTGCTGCTTTGAAAGAGCTGCTGCAGAAATGGTATGAAT - 10800
- G I A V L D M C A A L K E L L Q N G M N
- E L P S * I C V L L * K S C C R M V * M
- N C R L R Y V C C F E R A A A E W Y E W

FIG. 4 Cont'd

10801 - GGTCGTACTATCCTTGGTAGCACTATTTTAGAAGATGAGTTTACACCATTGATGTTGTT - 10860
- G R T I L G S T I L E D E F T P F D V V
- V V L S L V A L F * K M S L H H L M L L
- S Y Y P W * H Y F R R * V Y T I * C C *
10861 - AGACAATGCTCTGGTGTACCTTCCAAGGTAAGTTCAAGAAAATTGTTAAGGGCACTCAT - 10920
- R Q C S G V T F Q G K F K K I V K G T H
- D N A L V L P S K V S S R K L L R A L I
- T M L W C Y L P R * V Q E N C * G H S S
10921 - CATTGGATGCTTTTAACTTTCTTGACATCACTATTGATTCTTGTTCAAAGTACACAGTGG - 10980
- H W M L L T F L T S L L I L V Q S T Q W
- I G C F * L S * H H Y * F L F K V H S G
- L D A F N F L D I T I D S C S K Y T V V
10981 - TCACTGTTTTCTTTGTTTACGAGAATGCTTTCTTGCCATTACTCTGGTATTATGGCA - 11040
- S L F F F V Y E N A F L P F T L G I M A
- H C F S L F T R M L S C H L L L V L W Q
- T V F L C L R E C F L A I Y S W Y Y G N
11041 - ATTGCTGCATGTGCTATGCTGCTTGTGAAGCATAAGCAGCATTCTGTGCTTGTCTTG - 11100
- I A C A M L L V K H K H A F L C L F L
- L L H V L C C L L S I S T H S C A C F C
- C C M C Y A A C * A * A R I L V L V S V
11101 - TTACCTTCTCTGCAACAGTTGCTTACTTTAATATGGTCTACATGCCTGCTAGCTGGGTG - 11160
- L P S L A T V A Y F N M V Y M P A S W V
- Y L L L Q Q L L T L I W S T C L L A G *
- T F S C N S C L L * Y G L H A C * L G D
11161 - ATGCGTATCATGACATGGCTTGAATTGGCTGACACTAGCTTGTCTGGTTATAGGCTTAAG - 11220
- M R I M T W L E L A D T S L S G Y R L K
- C V S * H G L N W L T L A C L V I G L R
- A Y H D M A * I G * H * L V W L * A * G
11221 - GATTGTGTTATGTATGCTTCAGCTTTAGTTTTGCTTATTCTCATGACAGCTCGCACTGTT - 11280
- D C V M Y A S A L V L L I L M T A R T V
- I V L C M L Q L * F C L F S * Q L A L F
- L C Y V C F S F S F A Y S H D S S H C L
11281 - TATGATGCTGCTAGACGTGTTTGGACACTGATGAATGTCATTACACTTGTTTACAAA - 11340
- Y D D A A R R V W T L M N V I T L V Y K
- M M M L L D V F G H * * M S L H L F T K
- * * C C * T C L D T D E C H Y T C L Q S
11341 - GTCTACTATGGTAATGCTTTAGATCAAGCTATTTCCATGTGGGCCTTAGTTATTTCTGTA - 11400
- V Y Y G N A L D Q A I S M W A L V I S V
- S T M V M L * I K L F P C G P * L F L *
- L L W * C F R S S Y F H V G L S Y F C N
11401 - ACCTCTAACTATTCTGGTGTGTTACGACTATCATGTTTTTAGCTAGAGCTATAGTGT - 11460
- T S N Y S G V V T T I M F L A R A I V F
- P L T I L V S L R L S C F * L E L * C L
- L * L F W C R Y D Y H V F S * S Y S V C
11461 - GTGTGTGTTGAGTATTACCCATTGTTATTTATTACTGGCAACACCTTACAGTGTATCATG - 11520
- V C V E Y Y P L L F I T G N T L Q C I M
- C V L S I T H C Y L L L A T P Y S V S C
- V C * V L P I V I Y Y W Q H L T V Y H A
11521 - CTTGTTTATTGTTTCTTAGGCTATTGTTGCTGCTACTTTGGCCTTTTCTGTTTACTC - 11580
- L V Y C F L G Y C C C C Y F G L F C L L
- L F I V S * A I V A A A T L A F S V Y S
- C L L F L R L L L L L W P F L F T Q
11581 - AACCGTTACTTCAGGCTTACTCTGGTGTATGACTACTTGGTCTCTACACAAGAATT - 11640
- N R Y F R L T L G V Y D Y L V S T Q E F
- T V T S G L L L V F M T T W S L H K N L
- P L L Q A Y S W C L * L L G L Y T R I *
11641 - AGGTATATGAACCTCCAGGGGCTTTGCTCCTAAGAGTAGTATTGATGCTTTCAAGCTT - 11700
- R Y M N S Q G L L P P K S S I D A F K L
- G I * T P R G F C L L R V V L M L S S L
- V Y E L P G A F A S * E * Y * C F Q A *

FIG. 4 Cont'd

11701 - AACATTAAGTTGTTGGGTATTGGAGGTAAACCATGTATCAAGGTTGCTACTGTACAGTCT - 11760
- N I K L L G I G G K P C I K V A T V Q S
- T L S C W V L E V N H V S R L L L Y S L
- H * V V G Y W R * T M Y Q G C Y C T V *
11761 - AAAATGTCTGACGTAAAGTGCACATCTGTGGTACTGCTCTCGGTTCTTCAACAACCTTAGA - 11820
- K M S D V K C T S V V L L S V L Q Q L R
- K C L T * S A H L W Y C S R F F N N L E
- N V * R K V H I C G T A L G S S T T * S
11821 - GTAGAGTCATCTTCTAAATTGTGGGCACAATGTGTACAACCTCCACAATGATATTTCTTCTT - 11880
- V E S S S K L W A Q C V Q L H N D I L L
- * S H L L N C G H N V Y N S T M I F F L
- R V I F * I V G T M C T T P Q * Y S S C
11881 - GCAAAAGACACAACCTGAAGCTTTTCGAGAAGATGGTTTCTTTTGTCTGTTTGTCTATCC - 11940
- A K D T T E A F E K M V S L L S V L L S
- Q K T Q L K L S R R W F L F C L F C Y P
- K R H N * S F R E D G F S F V C F A I H
11941 - ATGCAGGGTGTGTAGACATTAATAGGTTGTGCGAGGAAATGCTCGATAACCGTGCTACT - 12000
- M Q G A V D I N R L C E E M L D N R A T
- C R V L * T L I G C A R K C S I T V L L
- A G C C R H * * V V R G N A R * P C Y S
12001 - CTTCAGGCTATTGCTTCAGAATTTAGTTCTTTACCATCATATGCCGCTTATGCCACTGCC - 12060
- L Q A I A S E F S S L P S Y A A Y A T A
- F R L L L Q N L V L Y H H M P L M P L P
- S G Y C F R I * F F T I I C R L C H C P
12061 - CAGGAGCCTATGAGCAGGCTGTAGCTAATGGTATTCTGAAGTCGTTCTCAAAAAGTTA - 12120
- Q E A Y E Q A V A N G D S E V V L K K L
- R R P M S R L * L M V I L K S F S K S *
- G G L * A G C S * W * F * S R S Q K V K
12121 - AAGAAATCTTTGAATGTGGCTAAATCTGAGTTTGACCGTGATGCTGCCATGCCACGCAAG - 12180
- K K S L N V A K S E F D R D A A M Q R K
- R N L * M W L N L S L T V M L P C N A S
- E I F E C G * I * V * P * C C H A T Q V
12181 - TTGGAAAAGATGGCAGATCAGGCTATGACCCAAATGTACAAACAGGCAAGATCTGAGGAC - 12240
- L E K M A D Q A M T Q M Y K Q A R S E D
- W K R W Q I R L * P K C T N R Q D L R T
- G K D G R S G Y D P N V Q T G K I * G Q
12241 - AAGAGGGCAAAAGTAAGTATGTGCTATGCAACAATGCTCTTCACTATGCTTAGGAAGCTT - 12300
- K R A K V T S A M Q T M L F T M L R K L
- R G Q K * L V L C K Q C S S L C L G S L
- E G K S N * C Y A N N A L H Y A * E A *
12301 - GATAATGATGCACTTAACAACATTATCAACAATGCGCGTGATGGTTGTGTTCCACTCAAC - 12360
- D N D A L N N I I N N A R D G C V P L N
- I M M H L T T L S T M R V M V V F H S T
- * * C T * Q H Y Q Q C A * W L C S T Q H
12361 - ATCATACCATTGACTACAGCAGCCAACTCATGGTTGTTGTCCTGATTATGGTACCTAC - 12420
- I I P L T T A A K L M V V V P D Y G T Y
- S Y H * L Q Q P N S W L L S L I M V P T
- H T I D Y S S Q T H G C C P * L W Y L Q
12421 - AAGAACACTTGTGATGGTAACACCTTTACATATGCATCTGCACTCTGGGAAATCCAGCAA - 12480
- K N T C D G N T F T Y A S A L W E I Q Q
- R T L V M V T P L H M H L H S G K S S K
- E H L * W * H L Y I C I C T L G N P A S
12481 - GTTGTGTGATGCGGATAGCAAGATTGTTCAACTTAGTGAAATTAACATGGACAATTCACCA - 12540
- V V D A D S K I V Q L S E I N M D N S P
- L L M R I A R L F N L V K L T W T I H Q
- C * C G * Q D C S T * * N * H G Q F T K
12541 - AATTGGCTTGGCCTCTTATTGTTACAGCTCTAAGAGCCAACCTCAGCTGTTAAACTACAG - 12600
- N L A W P L I V T A L R A N S A V K L Q
- I W L G L L L L Q L * E P T Q L L N Y R
- F G L A S Y C Y S S K S Q L S C * T T E

FIG. 4 Cont'd

12601 - AATAATGAAGTCCAGTCCAGTACGACAGATGTCCTGTGCGGCTGGTACCACACAA - 12660
- N N E L S P V A L R Q M S C A A G T T Q
- I M N * V Q * H Y D R C P V R L V P H K
- * * T E S S S T T T D V L C G W Y H T N
12661 - ACAGCTTGACTGATGACAATGCACTTGCCTACTATAACAATTCGAAGGGAGGTAGGTTT - 12720
- T A C T D D N A L A Y Y N N S K G G R F
- Q L V L M T M H L P T I T I R R E V G L
- S L Y * * Q C T C L L * Q F E G R * V C
12721 - GTGCTGGCATTACTATCAGACCACCAAGATCTCAAATGGGCTAGATTCCCTAAGAGTGAT - 12780
- V L A L L S D H Q D L K W A R F P K S D
- C W H Y Y Q T T K I S N G L D S L R V M
- A G I T I R P P R S Q M G * I P * E * W
12781 - GGTACAGGTACAATTTACACAGAAGTGAACCACTTGTAGGTTTGTACAGACACACCA - 12840
- G T G T I Y T E L E P P C R F V T D T P
- V Q V Q F T Q N W N H L V G L L Q T H Q
- Y R Y N L H R T G T T L * V C Y R H T K
12841 - AAAGGGCCTAAAGTGAATACCTGTACTTCATCAAAGGCTTAAACAACCTAAATAGAGGT - 12900
- K G P K V K Y L Y F I K G L N N L N R G
- K G L K * N T C T S S K A * T T * I E V
- R A * S E I L V L H Q R L K Q P K * R Y
12901 - ATGGTGCTGGGCGAGTTAGCTGTACAGTACGTCTTCAGGCTGGAAATGCTACAGAAGTA - 12960
- M V L G S L A A T V R L Q A G N A T E V
- W C W A V * L L Q Y V F R L E M L Q K Y
- G A G Q F S C Y S T S S G W K C Y R S T
12961 - CCTGCCAATTCAACTGTGCTTTCTCTGTGCTTTTGCAGTAGACCCTGCTAAAGCATAT - 13020
- P A N S T V L S F C A F A V D P A K A Y
- L P I Q L C F P S V L L Q * T L L K H I
- C Q F N C A F L L C F C S R P C * S I *
13021 - AAGGTATACCTAGCAAGTGGAGGACAACCAACTGTGTGAAGATGTTGTGTACA - 13080
- K D Y L A S G G Q P I T N C V K M L C T
- R I T * Q V E D N Q S P T V * R C C V H
- G L P S K W R T T N H Q L C E D V V Y T
13081 - CACACTGGTACAGGACAGGCAATTACTGTAACACCAGAAGCTAACATGGACCAAGAGTCC - 13140
- H T G T G Q A I T V T P E A N M D Q E S
- T L V Q D R Q L L * H Q K L T W T K S P
- H W Y R T G N Y C N T R S * H G P R V L
13141 - TTGGTGGTCTTCATGTTGTCTGTATTGTAGATGCCACATTGACCATCCAATCCTAAA - 13200
- F G G A S C C L Y C R C H I D H P N P K
- L V V L H V V C I V D A T L T I Q I L K
- W W C F M L S V L * M P H * P S K S * R
13201 - GGATTCTGTGACTTGAAAGGTAAGTACGTCCAAATACCTACCACTTGTGCTAATGACCCA - 13260
- G F C D L K G K Y V Q I P T T C A N D P
- D S V T * K V S T S K Y L P L V L M T Q
- I L * L E R * V R P N T Y H L C * * P S
13261 - GTGGGTTTTACACTTAGAAACACAGTCTGTACCGTCTGCGGAATGTGGAAGGTTATGGC - 13320
- V G F T L R N T V C T V C G M W K G Y G
- W V L H L E T Q S V P S A E C G K V M A
- G F Y T * K H S L Y R L R N V E R L W L
13321 - TGTAGTTGTGACCAACTCCGCGAACCTTGATGCAGTCTGCGGATGCATCAACGTTTTTA - 13380
- C S C D Q L R E P L M Q S A D A S T F L
- V V V T N S A N P * C S L R M H Q R F *
- * L * P T P R T L D A V C G C I N V F K
13381 - AACGGGTTTGCAGTGAAGTGCAGCCGCTTACACCGTGCGGCACAGGCACTAGTACTG - 13440
- N G F A V * V Q P V L H R A A Q A L V L
- T G L R C K C S P S Y T V R H R H * Y *
- R V C G V S A A R L T P C G T G T S T D
13441 - ATGTCGTCTACAGGCTTTTGATATTTACAACGAAAAAGTTGCTGGTTTTGCAAAGTTC - 13500
- M S S T G L L I F T T K K L L V L Q S S
- C R L Q G F * Y L Q R K S C W F C K V P
- V V Y R A F D I Y N E K V A G F A K F L

FIG. 4 Cont'd

13501 - TAAAACTAATTGCTGTCGCTTCCAGGAGAAGGATGAGGAAGGCAATTATTAGACTCTT - 13560
- * K L I A V A S R R R M R K A I Y * T L
- K N * L L S L P G E G * G R Q F I R L L
- K T N C C R F Q E K D E E G N L L D S Y
13561 - ACTTTGTAGTTAAGAGGCATACTATGTCTAACTACCAACATGAAGAGACTATTTATAACT - 13620
- T L * L R G I L C L T T N M K R L F I T
- L C S * E A Y Y V * L P T * R D Y L * L
- F V V K R H T M S N Y Q H E E T I Y N L
13621 - TGGTTAAAGATTGTCCAGCGTTGCTGTCCATGACTTTTCAAGTTTAGAGTAGATGGTG - 13680
- W L K I V Q R L L S M T F S S L E * M V
- G * R L S S G C C P * L F Q V * S R W *
- V K D C P A V A V H D F F K F R V D G D
13681 - ACATGGTACCACATATATCACGTCAGCGTCTAACTAAATACACAATGGCTGATTAGTCT - 13740
- T W Y H I Y H V S V * L N T Q W L I * S
- H G T T Y I T S A S N * I H N G * F S L
- M V P H I S R Q R L T K Y T M A D L V Y
13741 - ATGCTCTACGTCATTTTGATGAGGGTAATTGTGATACATTAAAAGAAATACTCGTCACAT - 13800
- M L Y V I L M R V I V I H * K K Y S S H
- C S T S F * * G * L * Y I K R N T R H I
- A L R H F D E G N C D T L K E I L V T Y
13801 - ACAATTGCTGTGATGATGATTATTTCAATAAGAAGGATTGGTATGACTTCGTAGAGAATC - 13860
- T I A V M M I I S I R R I G M T S * R I
- Q L L * * * L F Q * E G L V * L R R E S
- N C C D D D Y F N K K D W Y D F V E N P
13861 - CTGACATCTTACGCGTATATGCTAACTTAGGTGAGCGTGTACGCCAATCATTATTAAAGA - 13920
- L T S Y A Y M L T * V S V Y A N H Y * R
- * H L T R I C * L R * A C T P I I I K D
- D I L R V Y A N L G E R V R Q S L L K T
13921 - CTGTACAATTCTGCGATGCTATGCGTGATGCAGGCATTGTAGGCGTACTGACATTAGATA - 13980
- L Y N S A M L C V M Q A L * A Y * H * I
- C T I L R C Y A * C R H C R R T D I R *
- V Q F C D A M R D A G I V G V L T L D N
13981 - ATCAGGATCTTAATGGGAAGTGGTACGATTTCGGTGATTTCGTACAAGTAGCACCAGGCT - 14040
- I R I L M G T G T I S V I S Y K * H Q A
- S G S * W E L V R F R * F R T S S T R L
- Q D L N G N W Y D F G D F V Q V A P G C
14041 - GCGGAGTTCCTATTGTGGATTCAATTACTCATTGCTGATGCCCATCCTCACTTTGACTA - 14100
- A E F L L W I H I T H C * C P S S L * L
- R S S Y C G F I L L I A D A H P H F D *
- G V P I V D S Y Y S L L M P I L T L T R
14101 - GGGCATTTGGCTGCTGAGTCCCATATGGATGCTGATCTCGCAAACCACTTATTAAGTGGG - 14160
- G H W L L S P I W M L I S Q N H L L S G
- G I G C * V P Y G C * S R K T T Y * V G
- A L A A E S H M D A D L A K P L I K W D
14161 - ATTTGCTGAAATATGATTTTACGGAAGAGAGACTTTGTCTCTTCGACCGTTATTTTAAAT - 14220
- I C * N M I L R K R D F V S S T V I L N
- F A E I * F Y G R E R L L S L R P L F * I
- L L K Y D F Y T E R L C L F D R Y F K Y
14221 - ATTGGGACCAGACATACCATCCCAATTGTATTAACTGTTTGGATGATAGGTGTATCCTTC - 14280
- I G T R H T I P I V L T V W M I G V S F
- L G P D I P S Q L Y * L F G * * V Y P S
- W D Q T Y H P N C I N C L D D R C I L H
14281 - ATTGTGCAAACTTTAATGTGTTATTTTCTACTGTGTTTCCACCTACAAGTTTGGACCAC - 14340
- I V Q T L M C Y F L L C F H L Q V L D H
- L C K L * C V I F Y C V S T Y K F W T T
- C A N F N V L F S T V F P P T S F G P L
14341 - TAGTAAGAAAAATATTTGTAGATGGTGTTCCTTTTGTGTTTCAACTGGATACCATTTTC - 14400
- * * E K Y L * M V F L L L F Q L D T I F
- S K K N I C R W C S F C C F N W I P F S
- V R K I F V D G V P F V V S T G Y H F R

FIG. 4 Cont'd

14401 - GTGAGTTAGGAGTCGTACATAATCAGGATGTAAACTTACATAGCTCGCGTCTCAGTTTCA - 14460
- V S * E S Y I I R M * T Y I A R V S V S
- * V R S R T * S G C K L T * L A S Q F Q
- E L G V V H N Q D V N L H S S R L S F K
14461 - AGGAACTTTTAGTGATGCTGCTGATCCAGCTATGCATGCAGCTTCTGGCAATTTATGTC - 14520
- R N F * C M L L I Q L C M Q L L A I Y C
- G T F S V C C * S S Y A C S F W Q F I A
- E L L V Y A A D P A M H A A S G N L L L
14521 - TAGATAAACGCACTACATGCTTTTCAGTAGCTGCACTAACAAACAATGTTGCTTTTCAAA - 14580
- * I N A L H A F Q * L H * Q T M L L F K
- R * T H Y M L F S S C T N K Q C C F S N
- D K R T T C F S V A A L T N N V A F Q T
14581 - CTGTCAAACCCGGTAATTTTAATAAAGACTTTTATGACTTTGCTGTGTCTAAAGGTTTCT - 14640
- L S N P V I L I K T F M T L L C L K V S
- C Q T R * F * * R L L * L C C V * R F L
- V K P G N F N K D F Y D F A V S K G F F
14641 - TTAAGGAAGGAGTTCTGTTGAACTAAACACTTCTTCTTGCTCAGGATGGCAACGCTG - 14700
- L R K E V L L N * N T S S L L R M A T L
- * G R K F C * T K T L L L C S G W Q R C
- K E G S S V E L K H F F F A Q D G N A A
14701 - CTATCAGTGATTATGACTATTATCGTTATAATCTGCCAACATGTGTGATATCAGACAAC - 14760
- L S V I M T I I V I I C Q Q C V I S D N
- Y Q * L * L L S L * S A N N V * Y Q T T
- I S D Y D Y Y R Y N L P T M C D I R Q L
14761 - TCCTATTTCGTAGTTGAAGTTGTTGATAAATACTTTGATTGTTACGATGGTGGCTGTATTA - 14820
- S Y S * L K L L I N T L I V T M V A V L
- P I R S * S C * * I L * L L R W W L Y *
- L F V V E V V D K Y F D C Y D G G C I N
14821 - ATGCCAACCAAGTAATCGTTAACAATCTGGATAAATCAGCTGGTTTCCCATTTAATAAAT - 14880
- M P T K * S L T I W I N Q L V S H L I N
- C Q P S N R * Q S G * I S W F P I * * M
- A N Q V I V N N L D K S A G F P F N K W
14881 - GGGGTAAGGCTAGACTTTATTATGACTCAATGAGTTATGAGGATCAAGATGCACTTTTCG - 14940
- G V R L D F I M T Q * V M R I K M H F S
- G * G * T L L * L N E L * G S R C T F R
- G K A R L Y Y D S M S Y E D Q D A L F A
14941 - CGTATACTAAGCGTAATGTCATCCCTACTATAACTCAAATGAATCTTAAGTATGCCATTA - 15000
- R I L S V M S S L L * L K * I L S M P L
- V Y * A * C H P Y Y N S N E S * V C H *
- Y T K R N V I P T I T Q M N L K Y A I S
15001 - GTGCAAGAATAGAGCTCGCACCGTAGCTGGTGTCTCTATCTGTAGTACTATGACAAATA - 15060
- V Q R I E L A P * L V S L S V V L * Q I
- C K E * S S H R S W C L Y L * Y Y D K *
- A K N R A R T V A G V S I C S T M T N R
15061 - GACAGTTTCATCAGAAATTATTGAAGTCAATAGCCGCCACTAGAGGAGCTACTGTGGTAA - 15120
- D S F I R N Y * S Q * P P L E E L L W *
- T V S S E I I E V N S R H * R S Y C G N
- Q F H Q K L L K S I A A T R G A T V V I
15121 - TTGGAACAAGCAAGTTTACGGTGGCTGGCATAATATGTTAAAACTGTTTACAGTGATG - 15180
- L E Q A S F T V A G I I C * K L F T V M
- W N K Q V L R W L A * Y V K N C L Q * C
- G T S K F Y G G W H N M L K T V Y S D V
15181 - TAGAACTCCACACTTATGGGTGGGATTATCCAAAATGTGACAGAGCCATGCCTAACA - 15240
- * K L H T L W V G I I Q N V T E P C L T
- R N S T P Y G L G L S K M * Q S H A * H
- E T P H L M G W D Y P K C D R A M P N M
15241 - TGCTTAGGATAATGGCCTCTCTGTGTTCTTGCTCGAAACATAACACTTGCTGTAACCTAT - 15300
- C L G * W P L L F L L A N I T L A V T Y
- A * D N G L S C S C S Q T * H L L * L I
- L R I M A S L V L A R K H N T C C N L S

FIG. 4 Cont'd

15301 - CACACCGTTTCTACAGGTTAGCTAACGAGTGTGCGCAAGTATTAAGTGAGATGGTCATGT - 15360
- H T V S T G * L T S V R K Y * V R W S C
- T P F L Q V S * R V C A S I K * D G H V
- H R F Y R L A N E C A Q V L S E M V M C
15361 - GTGGCGGCTCACTATATGTTAAACCAGGTGGAACATCATCCGGTGATGCTACAACCTGCTT - 15420
- V A A H Y M L N Q V E H H P V M L Q L L
- W R L T I C * T R W N I I R * C Y N C L
- G G S L Y V K P G T S S G D A T T A Y
15421 - ATGCTAATAGTGTCTTTAACATTTGTCAAGCTGTTACAGCCAATGTAAATGCACTTCTTT - 15480
- M L I V S L T F V K L L Q P M * M H F F
- C * * C L * H L S S C Y S Q C K C T S F
- A N S V F N I C Q A V T A N V N A L L S
15481 - CAACTGATGGTAATAAGATAGCTGACAAGTATGTCCGCAATCTACAACACAGGCTCTATG - 15540
- Q L M V I R * L T S M S A I Y N T G S M
- N * W * * D S * Q V C P Q S T T Q A L *
- T D G N K I A D K Y V R N L Q H R L Y E
15541 - AGTGTCTCTATAGAAATAGGGATGTTGATCATGAATTCGTGGATGAGTTTACGCTTACC - 15600
- S V S I E I G M L I M N S W M S F T L T
- V S L * K * G C * S * I R G * V L R L P
- C L Y R N R D V D H E F V D E F Y A Y L
15601 - TGCCTAAACATTTCTCCATGATGATTCTTTCTGATGATGCCGTTGTGTGCTATAACAGTA - 15660
- C V N I S P * * F F L M M P L C A I T V
- A * T F L H D D S F * * C R C V L * Q *
- R K H F S M M I L S D D A V V C Y N S N
15661 - ACTATGCGGCTCAAGGTTTAGTAGCTAGCATTAAAGAACTTTAAGGCAGTTCTTTATTATC - 15720
- T M R L K V * * L A L R T L R Q F F I I
- L C G S R F S S * H * E L * G S S L L S
- Y A A Q G L V A S I K N F K A V L Y Y Q
15721 - AAAATAATGTGTCTGCTGAGGCAAAATGTTGACTGAGACTGACCTTACTAAAGGAC - 15780
- K I M C S C L R Q N V G L R L T L L K D
- K * C V H V * G K M L D * D * P Y * R T
- N N V F M S E A K C W T E T D L T K G P
15781 - CTCACGAATTTTGTCTACAGCATAAATGCTAGTTAAACAAGGAGATGATTACGTGTACC - 15840
- L T N F A H S I Q C * L N K E M I T C T
- S R I L L T A Y N A S * T R R * L R V P
- H E F C S Q H T M L V K Q G D D Y V Y L
15841 - TGCCTTACCCAGATCCATCAAGAATATTAGGCGCAGGCTGTTTGTGCGATGATATTGTCA - 15900
- C L T Q I H Q E Y * A Q A V L S M I L S
- A L P R S I K N I R R R L F C R * Y C Q
- P Y P D P S R I L G A G C F V D D I V K
15901 - AAACAGATGGTACACTTATGATTGAAAGGTTCTGTGCTACTGGCTATTGATGCTTACCCAC - 15960
- K Q M V H L * L K G S C H W L L M L T H
- N R W Y T Y D * K V R V T G Y * C L P T
- T D G T L M I E R F V S L A I D A Y P L
15961 - TTACAAAACATCCTAATCAGGAGTATGCTGATGTCTTCACTTGTATTTACAATACATTA - 16020
- L Q N I L I R S M L M S F T C I Y N T L
- Y K T S * S G V C * C L S L V F T I H *
- T K H P N Q E Y A D V F H L Y L Q Y I R
16021 - GAAAGTTACATGATGAGCTTACTGGCCACATGTTGGACATGTATTCCGTAATGCTAACTA - 16080
- E S Y M M S L L A T C W T C I P * C * L
- K V T * * A Y W P H V G H V F R N A N *
- K L H D E L T G H M L D M Y S V M L T N
16081 - ATGATAACACCTCAGGTACTGGGAACCTGAGTTTATGAGGCTATGTACACACCACATA - 16140
- M I T P H G T G N L S F M R L C T H H I
- * * H L T V L G T * V L * G Y V H T T Y
- D N T S R Y W E P E F Y E A M Y T P H T
16141 - CAGTCTTGCAGGCTGTAGGTGCTTGTATTGTGCAATTCACAGACTTCACTTCGTTGCG - 16200
- Q S C R L * V L V Y C A I H R L H F V A
- S L A G C R C L C I V Q F T D F T S L R
- V L Q A V G A C V L C N S Q T S L R C G

FIG. 4 Cont'd

16201 - GTGCCTGTATTAGGAGACCATTCCCTATGTTGCAAGTGCTGCTATGACCATGTCATTTCAA - 16260
- V P V L G D H S Y V A S A A M T M S F Q
- C L Y * E T I P M L Q V L L * P C H F N
- A C I R R P F L C C K C C Y D H V I S T
16261 - CATCACACAAATTAGTGTGTCTGTTAATCCCTATGTTTGCAATGCCCCAGGTTGTGATG - 16320
- H H T N * C C L L I P M F A M P Q V V M
- I T Q I S V V C * S L C L Q C P R L * C
- S H K L V L S V N P Y V C N A P G C D V
16321 - TCACTGATGTGACACAACCTGTATCTAGGAGGTATGAGCTATTATTGCAAGTCACATAAGC - 16380
- S L M * H N C I * E V * A I I A S H I S
- H * C D T T V S R R Y E L L L Q V T * A
- T D V T Q L Y L G G M S Y Y C K S H K P
16381 - CTCCCATAGTTTTCCATTATGTGCTAATGGTCAGGTTTTTGGTTTATACAAAACACAT - 16440
- L P L V F H Y V L M V R F L V Y T K T H
- S H * F S I M C * W S G F W F I Q K H M
- P I S F P L C A N G Q V F G L Y K N T C
16441 - GTGTAGGCAGTGACAAATGTCACTGACTTCAATGCGATAGCAACATGTGATTGGACTAATG - 16500
- V * A V T M S L T S M R * Q H V I G L M
- C R Q * Q C H * L Q C D S N M * L D * C
- V G S D N V T D F N A I A T C D W T N A
16501 - CTGGCGATTACATACTTGCCAACTTGTACTGAGAGACTCAAGCTTTTCGCAGCAGAAA - 16560
- L A I T Y L P T L V L R D S S F S Q Q K
- W R L H T C Q H L Y * E T Q A F R S R N
- G D Y I L A N T C T E R L K L F A A E T
16561 - CGCTCAAAGCCACTGAGGAAACATTTAAGCTGTATATGGTATTGCCACTGTACGCGAAG - 16620
- R S K P L R K H L S C H M V L P L Y A K
- A Q S H * G N I * A V I W Y C H C T R S
- L K A T E E T F K L S Y G I A T V R E V
16621 - TACTCTCTGACAGAGAATTGCATCTTTTCATGGGAGGTTGGAAAACCTAGACCACCATTGA - 16680
- Y S L T E N C I F H G R L E N L D H H *
- T L * Q R I A S F M G G W K T * T T I E
- L S D R E L H L S W E V G K P R P P L N
16681 - ACAGAACTATGTCTTTACTGGTTACCGTGTAACATAAAATAGTAAAGTACAGATTGGAG - 16740
- T E T M S L L V T V * L K I V K Y R L E
- Q K L C L Y W L P C N * K * * S T D W R
- R N Y V F T G Y R V T K N S K V Q I G E
16741 - AGTACACCTTTGAAAAGGTGACTATGGTGATGCTGTTGTGTACAGAGGTACTACGACAT - 16800
- S T P L K K V T M V M L L C T E V L R H
- V H L * K R * L W * C C C V Q R Y Y D I
- Y T F E K G D Y G D A V V Y R G T T T Y
16801 - ACAAGTTGAATGTTGGTGATTACTTTGTGTTGACATCTCACACTGTAATGCCACTTAGTG - 16860
- T S * M L V I T L C * H L T L * C H L V
- Q V E C W * L L C V D I S H C N A T * C
- K L N V G D Y F V L T S H T V M P L S A
16861 - CACCTACTCTAGTGCCACAAGAGCACTATGTGAGAATTACTGGCTGTACCCAACACTCA - 16920
- H L L * C H K S T M * E L L A C T Q H S
- T Y S S A T R A L Y C E N Y W L V P N T Q
- P T L V P Q E H Y V R I T G L Y P T L N
16921 - ACATCTCAGATGAGTTTTCTAGCAATGTTGCAAATTATCAAAGGTCGGCATGCAAAAGT - 16980
- T S Q M S F L A M L Q I I K R S A C K S
- H L R * V F * Q C C K L S K G R H A K V
- I S D E F S S N V A N Y Q K V G M Q K Y
16981 - ACTCTACACTCCAAGGACCACCTGGTACTGGTAAGAGTCATTTTGCCATCGGACTTGCTC - 17040
- T L H S K D H L V L V R V I L P S D L L
- L Y T P R T T W Y W * E S F C H R T C S
- S T L Q G P P G T G K S H F A I G L A L
17041 - TCTATTACCATCTGCTCGCATAGTGTATACGGCATGCTCTCATGCAGCTGTTGATGCCC - 17100
- S I T H L L A * C I R H A L M Q L L M P
- L L P I C S H S V Y G M L S C S C * C P
- Y Y P S A R I V Y T A C S H A A V D A L

FIG. 4 Cont'd

17101 - TATGTGAAAAGGCATTAAATATTTGCCCATAGATAAATGTAGTAGAATCATACCTGCGC - 17160
- Y V K R H * N I C P * I N V V E S Y L R
- M * K G I K I F A H R * M * * N H T C A
- C E K A L K Y L P I D K C S R I I P A R
17161 - GTGCGCGCTAGAGTGTTTTGATAAATTCAAAGTGAATTCAACACTAGAACAGTATGTTT - 17220
- V R A * S V L I N S K * I Q H * N S M F
- C A R R V F * * I Q S E F N T R T V C F
- A R V E C F D K F K V N S T L E Q Y V F
17221 - TCTGCACTGTAATGCATTGCCAGAACTGCTGACATTGTAGTCTTTGATGAAATCT - 17280
- S A L * M H C Q K Q L L T L * S L M K S
- L H C K C I A R N N C * H C S L * * N L
- C T V N A L P E T T A D I V V F D E I S
17281 - CTATGGCTACTAATTATGACTTGAGTGTGTCAATGCTAGACTTCGTGCAAACTACG - 17340
- L W L L I M T * V L S M L D F V Q N T T
- Y G Y * L * L E C C Q C * T S C K T L R
- M A T N Y D L S V V N A R L R A K H Y V
17341 - TCTATATTGGCGATCCTGCTCAATTACCAGCCCCCGCACATTGCTGACTAAAGGCACAC - 17400
- S I L A I L L N Y Q P P A H C * L K A H
- L Y W R S C S I T S P P H I A D * R H T
- Y I G D P A Q L P A P R T L L T K G T L
17401 - TAGAACCAGAATATTTTAATTCAGTGTGCAGACTTATGAAAACAATAGGTCCAGACATG - 17460
- * N Q N I L I Q C A D L * K Q * V Q T C
- R T R I F * F S V Q T Y E N N R S R H V
- E P E Y F N S V C R L M K T I G P D M F
17461 - TCCTTGGAACCTTGTGCGCTGTCTGCTGAAATTGTTGACACTGTGAGTGTCTTAGTTT - 17520
- S L E L V A V V L L K L L T L * V L * F
- P W N L S P L S C * N C * H C E C F S L
- L G T C R R C P A E I V D T V S A L V Y
17521 - ATGACAATAAGCTAAAAGCACACAAGGAGAAGTCACTCAATGCTTCAAAATGTTCTACA - 17580
- M T I S * K H T R R S Q L N A S K C S T
- * Q * A K S T Q G E V S S M L Q N V L Q
- D N K L K A H K E K S A Q C F K M F Y K
17581 - AAGGTGTTATTACACATGATGTTTCATCTGCAATCAACAGACCTCAAATAGGCGTTGTAA - 17640
- K V L L H M M F H L Q S T D L K * A L *
- R C Y Y T * C F I C N Q Q T S N R R C K
- G V I T H D V S S A I N R P Q I G V V R
17641 - GAGAATTTCTTACACGCAATCCTGCTTGAGAAAGCTGTTTTTATCTCACCTTATAATT - 17700
- E N F L H A I L L G E K L F L S H L I I
- R I S Y T Q S C L E K S C F Y L T L * F
- E F L T R N P A W R K A V F I S P Y N S
17701 - CACGAACGCTGTAGCTTCAAAATCTTAGGATTGCCTACGCAGACTGTTGATTCATCAC - 17760
- H R T L * L Q K S * D C L R R L L I H
- T E R C S F K N L R I A Y A D C * F I T
- Q N A V A S K I L G L P T Q T V D S S Q
17761 - AGGGTTCTGAATATGACTATGTCATATTCACACAACTACTGAAACAGCACACTCTTGTA - 17820
- R V L N M T M S Y S H K L L K Q H T L V
- G F * I * L C H I H T N Y * N S T L L *
- G S E Y D Y V I F T Q T T E T A H S C N
17821 - ATGTCAACCGTTTCAATGTGGCTATCACAAGGGCAAAATTTGGCATTGTTGTCATAATGT - 17880
- M S T V S M W L S Q G Q K L A F C A * C
- C Q P F Q C G Y H K G K N W H F V H N V
- V N R F N V A I T R A K I G I L C I M S
17881 - CTGATAGAGATCTTTATGACAACTGCAATTTACAAGTCTAGAAATACCACGTCGCAATG - 17940
- L I E I F M T N C N L Q V * K Y H V A M
- * * R S L * Q T A I Y K S R N T T S Q C
- D R D L Y D K L Q F T S L E I P R R N V
17941 - TGGCTACATTACAAGCAGAAAATGTAAGTGGACTTTTTAAGGACTGTAGTAAGATCATT - 18000
- W L H Y K Q K M * L D F L R T V V R S L
- G Y I T S R K C N W T F * G L * * D H Y
- A T L Q A E N V T G L F K D C S K I I T

FIG. 4 Cont'd

18001 - CTGGTCTTCATCCTACACAGGCACCTACACACCTCAGCGTTGATATAAAGTTCAAGACTG - 18060
- L V F I L H R H L H T S A L I * S S R L
- W S S S Y T G T Y T P Q R * Y K V Q D *
- G L H P T Q A P T H L S V D I K F K T E
18061 - AAGGATTATGTGTTGACATACCAGGCATACCAAAGGACATGACCTACCGTAGACTCATCT - 18120
- K D Y V L T Y Q A Y Q R T * P T V D S S
- R I M C * H T R H T K G H D L P * T H L
- G L C V D I P G I P K D M T Y R R L I S
18121 - CTATGATGGGTTTCAAAATGAATTACCAAGTCAATGGTTACCCTAATATGTTTATCACCC - 18180
- L * W V S K * I T K S M V T L I C L S P
- Y D G F Q N E L P S Q W L P * Y V Y H P
- M M G F K M N Y Q V N G Y P N M F I T R
18181 - GCGAAGAAGCTATTCGTCACGTTTCGTCGCGTGGATTGGCTTTGATGTAGAGGGCTGTCTATG - 18240
- A K K L F V T F V R G L A L M * R A V M
- R R S Y S S R S C V D W L * C R G L S C
- E E A I R H V R A W I G F D V E G C H A
18241 - CAACTAGAGATGCTGTGGGTACTAACCTACCTCTCCAGCTAGGATTTTCTACAGGTGTTA - 18300
- Q L E M L W V L T Y L S S * D F L Q V L
- N * R C C G Y * P T S P A R I F Y R C *
- T R D A V G T N L P L Q L G F S T G V N
18301 - ACTTAGTAGCTGTACCGACTGGTTATGTTGACACTGAAAATAACACAGAATTCACCAGAG - 18360
- T * * L Y R L V M L T L K I T Q N S P E
- L S S C T D W L C * H * K * H R I H Q S
- L V A V P T G Y V D T E N N T E F T R V
18361 - TTAATGCAAAACCTCCACCAGGTGACCAAGTTTAAACATCTTATACCACTCATGTATAAAG - 18420
- L M Q N L H Q V T S L N I L Y H S C I K
- * C K T S T R * P V * T S Y T T H V * R
- N A K P P P G D Q F K H L I P L M Y K G
18421 - GCTTGCCCTGGAATGTAGTGCGTATTAAGATAGTACAAATGCTCAGTGATACACTGAAAG - 18480
- A C P G M * C V L R * Y K C S V I H * K
- L A L E C S A Y * D S T N A Q * Y T E R
- L P W N V V R I K I V Q M L S D T L K G
18481 - GATTGTCAGACAGAGTCGTGTTTCGTCCTTTGGGCGCATGGCTTTGAGCTTACATCAATGA - 18540
- D C Q T E S C S S F G R M A L S L H Q *
- I V R Q S R V R P L G A W L * A Y I N E
- L S D R V V F V L W A H G F E L T S M K
18541 - AGTACTTTGTCAAGATTGGACCTGAAAGAACGTGTTGTCTGTGTGACAAACGTGCAACTT - 18600
- S T S R L D L K E R V V C V T N V Q L
- V L C Q D W T * K N V L S V * Q T C N L
- Y F V K I G P E R T C C L C D K R A T C
18601 - GCTTTTCTACTTCATCAGATACTTATGCCTGCTGGAATCATTCTGTGGGTTTTGACTATG - 18660
- A F L L H Q I L M P A G I I L W V L T M
- L F Y F I R Y L C L L E S F C G F * L C
- F S T S S D T Y A C W N H S V G F D Y V
18661 - TCTATAACCCATTATGATTGATGTTTCAGCAGTGGGGCTTTACGGGTAACCTTCAGAGTA - 18720
- S I T H L * L M F S S G A L R V T F R V
- L * P I Y D * C S A V G L Y G * P S E *
- Y N P F M I D V Q Q W G F T G N L Q S N
18721 - ACCATGACCAACATTGCCAGGTACATGGAAATGCACATGTGGCTAGTTGTGATGCTATCA - 18780
- T M T N I A R Y M E M H M W L V V M L S
- P * P T L P G T W K C T C G * L * C Y H
- H D Q H C Q V H G N A H V A S C D A I M
18781 - TGACTAGATGTTTAGCAGTCCATGAGTGCTTTGTTAAGCGCGTTGATTGGTCTGTTGAAT - 18840
- * L D V * Q S M S A L L S A L I G L L N
- D * M F S S P * V L C * A R * L V C * I
- T R C L A V H E C F V K R V D W S V E Y
18841 - ACCCTATTATAGGAGATGAAGTGAAGGTTAATTCTGCTTGCAGAAAAGTACAACACATGG - 18900
- T L L * E M N * G L I L L A E K Y N T W
- P Y Y R R * T E G * F C L Q K S T T H G
- P I I G D E L R V N S A C R K V Q H M V

FIG. 4 Cont'd

18901 - TTGTGAAGTCTGCATTGCTTGCTGATAAGTTTCCAGTTCTTCATGACATTGGAAATCCAA - 18960
- L * S L H C L L I S F Q F F M T L E I Q
- C E V C I A C * * V S S S S * H W K S K
- V K S A L L A D K F P V L H D I G N P K
18961 - AGGCTATCAAGTGTGTGCCTCAGGCTGAAGTAGAATGGAAGTTCTACGATGCTCAGCCAT - 19020
- R L S S V C L R L K * N G S S T M L S H
- G Y Q V C A S G * S R M E V L R C S A M
- A I K C V P Q A E V E W K F Y D A Q P C
19021 - GTAGTGACAAAGCTTACAAAATAGAGGAGCTCTTCTATTCTTATGCTACACATCAGGATA - 19080
- V V T K L T K * R S S S I L M L H I T I
- * * Q S L Q N R G A L L F L C Y T S R *
- S D K A Y K I E E L F Y S Y A T H H D K
19081 - AATTCAGTATGGTGTGTTGTTGTTTGGGAATTGTAACGTTGATCGTTACCCAGCCAATG - 19140
- N S L M V F V C F G I V T L I V T Q P M
- I H * W C L F V L E L * R * S L P S Q C
- F T D G V C L F W N C N V D R Y P A N A
19141 - CAATTGTGTGTAGGTTTGACACAAGAGTCTTGTCAAACCTGAACTTACCAGGCTGTGATG - 19200
- Q L C V G L T Q E S C Q T * T Y Q A V M
- N C V * V * H K S L V K L E L T R L * W
- I V C R F D T R V L S N L N L P G C D G
19201 - GTGGTAGTTGTATGTGAATAAGCATGCATTCCACACTCCAGCTTTCGATAAAAGTGCAT - 19260
- V V V C M * I S M H S T L Q L S I K V H
- W * F V C E * A C I P H S S F R * K C I
- G S L Y V N K H A F H T P A F D K S A F
19261 - TTACTAATTTAAAGCAATTGCCTTTCTTTTACTATTCTGATAGTCCTTGTGAGTCTCATG - 19320
- L L I * S N C L S F T I L I V L V S L M
- Y * F K A I A F L L L F * * S L * V S W
- T N L K Q L P F F Y Y S D S P C E S H G
19321 - GCAAACAAGTAGTGTCCGATATTGATTATGTTCCACTCAAATCTGCTACGTGTATTACAC - 19380
- A N K * C R I L I M F H S N L L R V L H
- Q T S S V G Y * L C S T Q I C Y V Y Y T
- K Q V V S D I D Y V P L K S A T C I T R
19381 - GATGCAATTTAGGTGGTGTGTTTGCAGACACCATGCAAATGAGTACCGACAGTACTTGG - 19440
- D A I * V V L F A D T M Q M S T D S T W
- M Q F R W C C L Q T P C K * V P T V L G
- C N L G G A V C R H H A N E Y R Q Y L D
19441 - ATGCATATAATATGATGATTTCTGCTGGATTAGCCTATGGATTACAAACAATTTGATA - 19500
- M H I I * * F L L D L A Y G F T N N L I
- C I * Y D D F C W I * P M D L Q T I * Y
- A Y N M M I S A G F S L W I Y K Q F D T
19501 - CTTATAACCTGTGGAATACATTTACCAGGTTACAGAGTTAGAAAATGTGGCTTATAATG - 19560
- L I T C G I H L P G Y R V * K M W L I M
- L * P V E Y I Y Q V T E F R K C G L * C
- Y N L W N T F T R L Q S L E N V A Y N V
19561 - TTGTTAATAAAGGACACTTTGATGGACACGCCGCGAAGCACCTGTTTCCATCATTAATA - 19620
- L L I K D T L M D T P A K H L F P S L I
- C * * R T L * W T R R R S T C F H H * *
- V N K G H F D G H A G E A P V S I I N N
19621 - ATGCTGTTTACACAAAGGTAGATGGTATTGATGTGGAGATCTTTGAAAATAAGACAACAC - 19680
- M L F T Q R * M V L M W R S L K I R Q H
- C C L H K G R W Y * C G D L * K * D N T
- A V Y T K V D G I D V E I F E N K T T L
19681 - TTCCTGTTAATGTTGCATTGAGCTTTGGGCTAAGCGTAACATTAAACCAGTGCCAGAGA - 19740
- F L L M L H L S F G L S V T L N Q C Q R
- S C * C C I * A L G * A * H * T S A R D
- P V N V A F E L W A K R N I K P V P E I
19741 - TTAAGATACTCAATAATTTGGGTGTTGATATCGCTGCTAATACTGTAATCTGGGACTACA - 19800
- L R Y S I I W V L I S L L I L * S G T T
- * D T Q * F G C * Y R C * Y C N L G L Q
- K I L N N L G V D I A A N T V I W D Y K

FIG. 4 Cont'd

19801 - AAAGAGAAGCCCCAGCACATGTATCTACAATAGGTGTCTGCACAATGACTGACATTGCCA - 19860
- K E K P Q H M Y L Q * V S A Q * L T L P
- K R S P S T C I Y N R C L H N D * H C Q
- R E A P A H V S T I G V C T M T D I A K
19861 - AGAAACCTACTGAGAGTGCTTGTCTTCACTTACTGTCTTGTGATGGTAGAGTGGAAG - 19920
- R N L L R V L V L H L L S C L M V E W K
- E T Y * E C L F F T Y C L V * W * S G R
- K P T E S A C S S L T V L F D G R V E G
19921 - GACAGGTAGACCTTTTGTAGAAACGCCCGTAATGGTGTGTTTAAATAACAGAAGGTTCACTCA - 19980
- D R * T F L E T P V M V F * * Q K V Q S
- T G R P F * K R P * W C F N N R R F S Q
- Q V D L F R N A R N G V L I T E G S V K
19981 - AAGGTCTAACACCTTCAAAGGGACCAGCACAAGCTAGCGTCAATGGAGTCACATTAATTG - 20040
- K V * H L Q R D Q H K L A S M E S H * L
- R S N T F K G T S T S * R Q W S H I N W
- G L T P S K G P A S V N G V T L I G
20041 - GAGATCAGTAAAAACACAGTTTAACTACTTTAAGAAAGTAGACGGCATTATTCAACAGT - 20100
- E N Q * K H S L T T L R K * T A L F N S
- R I S K N T V * L L * E S R R H Y S T V
- E S V K T Q F N Y F K K V D G I I Q Q L
20101 - TGCCTGAAACCTACTTTACTCAGAGCAGAGACTTAGAGGATTTTAAAGCCAGATCACAAA - 20160
- C L K P T L L R A E T * R I L S P D H K
- A * N L L Y S E Q R L R G F * A Q I T N
- P E T Y F T Q S R D L E D F K P R S Q M
20161 - TGGAAACTGACTTTCTCGAGCTCGCTATGGATGAATTCATACAGCGATATAAGCTCGAGG - 20220
- W K L T F S S S L W M N S Y S D I S S R
- G N * L S R A R Y G * I H T A I * A R G
- E T D F L E L A M D E F I Q R Y K L E G
20221 - GCTATGCCTTCGAACACATCGTTTATGGAGATTTCACTGATGGACAACCTTGGCGGTCTTC - 20280
- A M P S N T S F M E I S V M D N L A V F
- L C L R T H R L W R F Q S W T T W R S S
- Y A F E H I V Y G D F S H G Q L G G L H
20281 - ATTTAATGATAGGCTTAGCCAAGCGCTCACAAGATTCACCACTTAAATTAGAGGATTTTA - 20340
- I * * A * P S A H K I H H L N * R I L
- F N D R L S Q A L T R F T T * I R G F Y
- L M I G L A K R S Q D S P L K L E D F I
20341 - TCCCTATGGACAGCACAGTGAAAAATTACTTCATAACAGATGCGCAACAGGTTTCATCAA - 20400
- S L W T A Q * K I T S * Q M R K Q V H Q
- P Y G Q H S E K L L H N R C A N R F I K
- P M D S T V K N Y F I T D A Q T G S S K
20401 - AATGTGTGTGTCTGTGATTGATCTTTTACTTGATGACTTTGTGAGATAATAAAGTCAC - 20460
- N V C V L * L I F Y L M T L S R * * S H
- M C V F C D * S F T * * L C R D N K V T
- C V C S V I D L L L D D F V E I I K S Q
20461 - AAGATTTGTGAGTGATTTCAAAAGTGGTCAAGGTTACAATTGACTATGCTGAAATTTTCAT - 20520
- K I C Q * F Q K W S R L Q L T M L K F H
- R F V S D F K S G Q G Y N * L C * N F I
- D L S V I S K V V K V T I D Y A E I S F
20521 - TCATGCTTTGGTGTAAAGGATGGACATGTTGAAACCTTCTACCCAAAACCTACAAGCAAGTC - 20580
- S C F G V R M D M L K P S T Q N Y K Q V
- H A L V * G W T C * N L L P K T T S K S
- M L W C K D G H V E T F Y P K L Q A S Q
20581 - AAGCGTGGCAACCAGGTGTTGCGATGCCTAACTTGTACAAGATGCAAGAATGCTTCTTG - 20640
- K R G N Q V L R C L T C T R C K E C F L
- S V A T R C C D A * L V Q D A K N A S *
- A W Q P G V A M P N L Y K M Q R M L L E
20641 - AAAAGTGTGACCTTCAGAATTATGGTGAAAATGCTGTTATACCAAAAGGAATAATGATGA - 20700
- K S V T F R I M V K M L L Y Q K E * * *
- K V * P S E L W * K C C Y T K R N N D E
- K C D L Q N Y G E N A V I P K G I M M N

FIG. 4 Cont'd

20701 - ATGTCGCAAAGTATACTCAACTGTGTCAATACTTAAATACACTTACTTTAGCTGTACCCCT - 20760
- M S Q S I L N C V N T * I H L L * L Y P
- C R K V Y S T V S I L K Y T Y F S C T L
- V A K Y T Q L C Q Y L N T L T L A V P Y
20761 - ACAACATGAGAGTTATTCACTTTGGTCTGGCTCTGATAAAGGAGTTGCACCAGGTACAG - 20820
- T T * E L F T L V L A L I K E L H Q V Q
- Q H E S Y S L W C W L * * R S C T R Y S
- N M R V I H F G A G S D K G V A P G T A
20821 - CTGTGCTCAGACAATGGTTGCCAACTGGCACACTACTTGTGATTGAGATCTTAATGACT - 20880
- L C S D N G C Q L A H Y L S I Q I L M T
- C A Q T M V A N W H T T C R F R S * * L
- V L R Q W L P T G T L L V D S D L N D F
20881 - TCGTCTCCGACGCAGATTCTACTTTAATTGGAGACTGTGCAACAGTACATACGGCTAATA - 20940
- S S P T Q I L L * L E T V Q Q Y I R L I
- R L R R R F Y F N W R L C N S T Y G * *
- V S D A D S T L I G D C A T V H T A N K
20941 - AATGGGACCTTATTATTAGCGATATGTATGACCCTAGGACCAACATGTGACAAAAGAGA - 21000
- N G T L L L A I C M T L G P N M * Q K R
- M G P Y Y * R Y V * P * D Q T C D K R E
- W D L I I S D M Y D P R T K H V T K E N
21001 - ATGACTCTAAAGAAGGGTTTTCACTTATCTGTGTGGATTATATAAAGCAAAACTAGCCC - 21060
- M T L K K G F S L I C V D L * S K N * P
- * L * R R V F H L S V W I Y K A K T S P
- D S K E G F F T Y L C G F I K Q K L A L
21061 - TGGGTGGTTCTATAGCTGTAAAGATAACAGAGCATTCTTGAATGCTGACCTTTACAGC - 21120
- W V V L * L * R * Q S I L G M L T F T S
- G W F Y S C K D N R A F L E C * P L Q A
- G G S I A V K I T E H S W N A D L Y K L
21121 - TTATGGGCCATTTCTCATGGTGGACAGCTTTTGTACAAATGTAAATGCATCATCATCGG - 21180
- L W A I S H G G Q L L L Q M * M H H H R
- Y G P F L M V D S F C Y K C K C I I I G
- M G H F S W W T A F V T N V N A S S S E
21181 - AAGCATTTTAAATGGGGCTAACTATCTTGGCAAGCCGAAGGAACAAATTGATGGCTATA - 21240
- K H F * L G L T I L A S R R N K L M A I
- S I F N W G * L S W Q A E G T N * W L Y
- A F L I G A N Y L G K P K E Q I D G Y T
21241 - CCATGCATGCTAACTACATTTTCTGGAGGAACACAATCCTATCCAGTTGTCTTCTCTATT - 21300
- P C M L T T F S G G T Q I L S S C L P I
- H A C * L H F L E E H K S Y P V V F L F
- M H A N Y I F W R N T N P I Q L S S Y S
21301 - CACTCTTTGACATGAGCAAATTCCTCTTAAATTAAGAGGAACTGCTGTAATGTCTCTTA - 21360
- H S L T * A N F L L N * E E L L * C L L
- T L * H E Q I S S * I K R N C C N V S *
- L F D M S K F P L K L R G T A V M S L K
21361 - AGGAGAATCAAATCAATGATATGATTATTCTCTCTTGAAAAAGGTAGGCTTATCATA - 21420
- R R I K S M I * F I L F W K K V G L S L
- G E S N Q * Y D L F S S G K R * A Y H *
- E N Q I N D M I Y S L L E K G R L I I R
21421 - GAGAAAAACAACAGAGTTGTGGTTTCAAGTGATATTCTTGTAAACAACTAAACGAACATGT - 21480
- E K T T E L W F Q V I F L L T T K R T C
- R K Q Q S C G F K * Y S C * Q L N E H V
- E N N R V V V S S D I L V N N * T N M F
21481 - TTATTTTCTTATTATTCTTACTCTCACTAGTGGTAGTGACCTTGACCGGTGCACCACTT - 21540
- L F S Y Y F L L S L V V V T L T G A P L
- Y F L I I S Y S H * W * * P * P V H H F
- I F L L F L T L T S G S D L D R C T T F
21541 - TTGATGATGTTCAAGCTCCTAATTACACTCAACATACTTCATCTATGAGGGGGGTTTACT - 21600
- L M M F K L I T L N I L H L * G G F T
- * * C S S S * L H S T Y F I Y E G G L L
- D D V Q A P N Y T Q H T S S M R G V Y Y

FIG. 4 Cont'd

21601 - ATCCTGATGAAATTTTATGATCAGACACTCTTTATTTAACTCAGGATTTATTTCTCCAT - 21660
- I L M K F L D Q T L F I * L R I Y F F H
- S * * N F * I R H S L F N S G F I S S I
- P D E I F R S D T L Y L T Q D L F L P F
21661 - TTTATTCTAATGTTACAGGGTTTCATACTATTAATCATACGTTTGACAACCCTGTCATAC - 21720
- F I L M L Q G F I L L I I R L T T L S Y
- L F * C Y R V S Y Y * S Y V * Q P C H T
- Y S N V T G F H T I N H T F D N P V I P
21721 - CTTTAAAGGATGGTATTTATTTTGCTGCCACAGAGAAATCAAATGTTGTCCTGGTGGG - 21780
- L L R M V F I L L P Q R N Q M L S V V G
- F * G W Y L F C C H R E I K C C P W L G
- F K D G I Y F A A T E K S N V V R G W V
21781 - TTTTGGTTCTACCATGAACAAGTCACAGTCGGTGATTATTATTAACAATTCTACTA - 21840
- F L V L P * T T S H S R * L L L T I L L
- F W F Y H E Q Q V T V G D Y Y * Q F Y *
- F G S T M N N K S Q S V I I I N N S T N
21841 - ATGTTGTTATACGAGCATGTAACTTGAATTGTGTGACAACCCTTTCTTTGCTGTTTCTA - 21900
- M L L Y E H V T L N C V T T L S L L F L
- C C Y T S M * L * I V * Q P F L C C F *
- V V I R A C N F E L C D N P F F A V S K
21901 - AACCCATGGGTACACAGACACATACTATGATATTCGATAATGCATTAAATGCACATTCG - 21960
- N P W V H R H I L * Y S I M H L I A L S
- T H G Y T D T Y Y D I R * C I * L H F R
- P M G T Q T H T M I F D N A F N C T F E
21961 - AGTACATATCTGATGCCCTTTTCGCTTGATGTTTCAGAAAAGTCAGGTAATTTAAACACT - 22020
- S T Y L M P F R L M F Q K S Q V I L N T
- V H I * C L F A * C F R K V R * F * T L
- Y I S D A F S L D V S E K S G N F K H L
22021 - TACGAGAGTTTGTGTTTAAAAATAAAGATGGGTTTCTCTATGTTTATAAGGGCTATCAAC - 22080
- Y E S L C L K I K M G F S M F I R A I N
- T R V C V * K * R W V S L C L * G L S T
- R E F V F K N K D G F L Y V Y K G Y Q P
22081 - CTATAGATGTAGTTCGTGATCTACCTTCTGGTTTAAACACTTTGAAACCTATTTTAAAGT - 22140
- L * M * F V I Y L L V L T L * N L F L S
- Y R C S S * S T F W F * H F E T Y F * V
- I D V V R D L P S G F N T L K P I F K L
22141 - TGCCTCTTGGTATTAACATTACAAATTTTAGAGCCATTCTTACAGCCTTTTCACCTGCTC - 22200
- C L L V L T L Q I L E P F L Q P F H L L
- A S W Y * H Y K F * S H S Y S L F T C S
- P L G I N I T N F R A I L T A F S P A Q
22201 - AAGACACTTGGGGCAGTCAGCTGCAGCCTATTTTGTGTTGCTATTTAAAGCCAACATACAT - 22260
- K T L G A R Q L Q P I L L A I * S Q L H
- R H L G H V S C S L F C W L F K A N Y I
- D T W G T S A A A Y F V G Y L K P T T F
22261 - TTATGCTCAAGTATGATGAAAATGGTACAATCACAGATGCTGTTGATTGTTCTCAAAATC - 22320
- L C S S M M K M V Q S Q M L L I V L K I
- Y A Q V * * K W Y N H R C C * L F S K S
- M L K Y D E N G T I T D A V D C S Q N P
22321 - CACTTGCTGAACCTCAAATGCTCTGTTAAGAGCTTTGAGATTGACAAAGGAATTTACCAGA - 22380
- H L L N S N A L L R A L R L T K E F T R
- T C * T Q M L C * E L * D * Q R N L P D
- L A E L K C S V K S F E I D K G I Y Q T
22381 - CCTCTAATTTCAGGGTTGTTCCCTCAGGAGATGTTGTGAGATTCCCTAATATTACAAACT - 22440
- P L I S G L F P Q E M L * D S L I L Q T
- L * F Q G C S L R R C C E I P * Y Y K L
- S N F R V V P S G D V V R F P N I T N L
22441 - TGTGTCCTTTTGGAGAGGTTTTAATGCTACTAAATCCCTTCTGTCTATGCATGGGAGA - 22500
- C V L L E R F L M L L N S L L S M H G R
- V S F W R G F * C Y * I P F C L C M G E
- C P F G E V F N A T K F P S V Y A W E R

FIG. 4 Cont'd

22501 - GAAAAAAATTCTAATTGTGTGCTGATTACTCTGTGCTCTACAACCTCAACATTTTTTT - 22560
- E K K F L I V L L I T L C S T T Q H F F
- K K N F * L C C * L L C A L Q L N I F F
- K K I S N C V A D Y S V L Y N S T F F S
22561 - CAACCTTTAAGTGCTATGGCGTTTCTGCCACTAAGTTGAATGATCTTTGCTTCTCCAATG - 22620
- Q P L S A M A F L P L S * M I F A S P M
- N L * V L W R F C H * V E * S L L L Q C
- T F K C Y G V S A T K L N D L C F S N V
22621 - TCTATGCAGATTCTTTTGTAGTCAAGGGAGATGATGTAAGACAAATAGCGCCAGGACAAA - 22680
- S M Q I L L * S R E M M * D K * R Q D K
- L C R F F C S Q G R * C K T N S A R T N
- Y A D S F V V K G D D V R Q I A P G Q T
22681 - CTGGTGTTATTGCTGATTATAATTATAAATGCCAGATGATTCATGGGTTGTGTCCTTG - 22740
- L V L L L I I I N C Q M I S W V V S L
- W C Y C * L * L * I A R * F H G L C P C
- G V I A D Y N Y K L P D D F M G C V L A
22741 - CTTGGAATACTAGGAACATTGATGCTACTTCAACTGGTAATTATAATTATAAATATAGGT - 22800
- L G I L G T L M L L Q L V I I I I N I G
- L E Y * E H * C Y F N W * L * L * I * V
- W N T R N I D A T S T G N Y N Y K Y R Y
22801 - ATCTTAGACATGGCAAGCTTAGGCCCTTTGAGAGAGACATATCTAATGTGCCTTTCTCCC - 22860
- I L D M A S L G P L R E T Y L M C L S P
- S * T W Q A * A L * E R H I * C A F L P
- L R H G K L R P F E R D I S N V P F S P
22861 - CTGATGGCAAACCTTGCACCCACCTGCTCTTAATTGTTATTGGCCATTAAATGATTATG - 22920
- L M A N L A P H L L L I V I G H * M I M
- * W Q T L H P T C S * L L L A I K * L W
- D G K P C T P P A L N C Y W P L N D Y G
22921 - GTTTTACACCACTACTGGCATTGGCTACCAACCTTACAGAGTTGTAGTACTTTCTTTTG - 22980
- V F T P L L A L A T N L T E L * Y F L L
- F L H H Y W H W L P T L Q S C S T F F *
- F Y T T T G I G Y Q P Y R V V V L S F E
22981 - AACTTTTAAATGCACCGGCCACGGTTTGTGGACCAAAATTATCCACTGACCTTATTAAGA - 23040
- N F * M H R P R F V D Q N Y P L T L L R
- T F K C T G H G L W T K I I H * P Y * E
- L L N A P A T V C G P K L S T D L I K N
23041 - ACCAGTGTGTCAATTTTAAATTTTAAATGGACTCACTGGTACTGGTGTGTTAACTCCTTCTT - 23100
- T S V S I L I L M D S L V L V C * L L L
- P V C Q F * F * W T H W Y W C V N S F F
- Q C V N F N F N G L T G T G V L T P S S
23101 - CAAAGAGATTTCAACCATTTCAACAATTTGGCCGTGATGTTTCTGATTTCACTGATTCCG - 23160
- Q R D F N H F N N L A V M F L I S L I P
- K E I S T I S T I W P * C F * F H * F R
- K R F Q P F Q Q F G R D V S D F T D S V
23161 - TTCGAGATCCTAAAACATCTGAAATATTAGACATTTACCTTGCTCTTTTGGGGGTGTAA - 23220
- F E I L K H L K Y * T F H L A L L G V *
- S R S * N I * N I R H F T L L F W G C K
- R D P K T S E I L D I S P C S F G G V S
23221 - GTGTAATTACACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTCTATATCAAGATGTTA - 23280
- V * L H L E Q M L H L K L L F Y I K M L
- C N Y T W N K C F I * S C C S I S R C *
- V I T P G T N A S S E V A V L Y Q D V N
23281 - ACTGCACTGATGTTTCTACAGCAATTCATGCAGATCAACTCACACCAGCTTGGCGCATAT - 23340
- T A L M F L Q Q F M Q I N S H Q L G A Y
- L H * C F Y S N S C R S T H T S L A H I
- C T D V S T A I H A D Q L T P A W R I Y
23341 - ATTCTACTGGAAACAATGTATTCCAGACTCAAGCAGGCTGTCTTATAGGAGCTGAGCATG - 23400
- I L L E T M Y S R L K Q A V L * E L S M
- F Y W K Q C I P D S S R L S Y R S * A C
- S T G N N V F Q T Q A G C L I G A E H V

FIG. 4 Cont'd

23401 - TCGACACTTCTTATGAGTGCACATTCTATTGGAGCTGGCATTGTGCTAGTTACCATA - 23460
- S T L L M S A T F L L E L A F V L V T I
- R H F L * V R H S Y W S W H L C * L P Y
- D T S Y E C D I P I G A G I C A S Y H T
23461 - CAGTTTCTTTATTACGTAGTACTAGCCAAAAATCTATTGTGGCTTATACTATGTCTTTAG - 23520
- Q F L Y Y V V L A K N L L W L I L C L *
- S F F I T * Y * P K I Y C G L Y Y V F R
- V S L L R S T S Q K S I V A Y T M S L G
23521 - GTGCTGATAGTTCAATTGCTTACTCTAATAACACCATTGCTATACCTACTAACTTTTCAA - 23580
- V L I V Q L L T L I T P L L Y L L T F Q
- C * * F N C L L * * H H C Y T Y * L F N
- A D S S I A Y S N N T I A I P T N F S I
23581 - TTAGCATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCTCCGTAGATTGTAATA - 23640
- L A L L Q K * C L F L W L K P P * I V I
- * H Y Y R S N A C F Y G * N L R R L * Y
- S I T T E V M P V S M A K T S V D C N M
23641 - TGTACATCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCCAATATGGTAGCTTTT - 23700
- C T S A E I L L N V L I C F S N M V A F
- V H L R R F Y * M C * F A S P I W * L L
- Y I C G D S T E C A N L L L Q Y G S F C
23701 - GCACACAATAAATCGTGCCTCTCAGGTATTGCTGCTGAACAGGATCGCAACACACGTG - 23760
- A H N * I V H S Q V L L L N R I A T H V
- H T T K S C T L R Y C C * T G S Q H T *
- T Q L N R A L S G I A A E Q D R N T R E
23761 - AAGTGTTCTGCTCAAGTCAAACAAATGTACAAAACCCCACTTTGAAATATTTTGGTGGTT - 23820
- K C S L K S N K C T K P Q L * N I L V V
- S V R S S Q T N V Q N P N F E I F W W F
- V F A Q V K Q M Y K T P T L K Y F G G F
23821 - TTAATTTTTTCAAAATATTACCTGACCTCTAAAGCCCACTAAGAGGTCTTTTATTGAGG - 23880
- L I F H K Y Y L T L * S Q L R G L L L R
- * F F T N I T * P S K A N * E V F Y * G
- N F S Q I L P D P L K P T K R S F I E D
23881 - ACTTGCTCTTAATAAGGTGACACTCGCTGATGCTGGCTTCATGAAGCAATATGGCGAAT - 23940
- T C S L I R * H S L M L A S * S N M A N
- L A L * * G D T R * C W L H E A I W R M
- L L F N K V T L A D A G F M K Q Y G E C
23941 - GCCTAGGTGATATTAATGCTAGAGATCTCATTGTGCGCAGAAGTTCAATGGACTTACAG - 24000
- A * V I L M L E I S F V R R S S M D L Q
- P R * Y * C * R S H L C A E V Q W T Y S
- L G D I N A R D L I C A Q K F N G L T V
24001 - TGTGCCCACCTCTGCTCACTGATGATGATTGCTGCCTACACTGCTGCTCTAGTTAGTG - 24060
- C C H L C S L M I * L L P T L L L * L V
- V A T S A H * * Y D C C L H C C S S * W
- L P P L L T D D M I A A Y T A A L V S G
24061 - GTACTGCCACTGCTGGATGGACATTGGTGCTGGCGCTGCTCTTCAAATACCTTTTGCTA - 24120
- V L P L L D G H L V L A L L F K Y L L L
- Y C H C W M D I W C W R C S S N T F C Y
- T A T A G W T F G A G A A L Q I P F A M
24121 - TGCAAATGGCATATAGGTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACC - 24180
- C K W H I G S M A L E L P K M F S M R T
- A N G I * V Q W H W S Y P K C S L * E P
- Q M A Y R F N G I G V T Q N V L Y E N Q
24181 - AAAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATCAAGAATCACTTACAA - 24240
- K N K S P T N L T R R L V K F K N H L Q
- K T N R Q P I * Q G D * S N S R I T Y N
- K Q I A N Q F N K A I S Q I Q E S L T T
24241 - CAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGAATGCTCAAGCATTAA - 24300
- Q H Q L H W A S C K T L L T R M L K H *
- N I N C I G Q A A R R C * P E C S S I K
- T S T A L G K L Q D V V N Q N A Q A L N

FIG. 4 Cont'd

24301 - ACACACTTGTAAACAACCTAGCTCTAATTTTGGTGCAATTTCAGGTGTGCTAAATGATA - 24360
- T H L L N N L A L I L V Q F Q V C * M I
- H T C * T T * L * F W C N F K C A K * Y
- T L V K Q L S S N F G A I S S V L N D I
24361 - TCCTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATTACAGGCA - 24420
- S F R D L I K S R R R Y K L T G * L Q: A
- P F A T * * S R G G G T N * Q V N Y R Q
- L S R L D K V E A E V Q I D R L I T G R
24421 - GACTTCAAAGCCTTCAAACCTATGTAACACAACAATAATCAGGGCTGCTGAAATCAGGG - 24480
- D F K A F K P M * H N N * S G L L K S G
- T S K P S N L C N T T T N Q G C * N Q G
- L Q S L Q T Y V T Q Q L I R A A E I R A
24481 - CTTCTGCTAATCTTGCTGCTACTAAATGTCTGAGTGTGTTCTTGGACAATCAAAAAGAG - 24540
- L L L I L L K C L S V F L D N Q K E
- F C * S C C Y * N V * V C S W T I K K S
- S A N L A A T K M S E C V L G Q S K R V
24541 - TTGACTTTTGTGAAAGGGCTACCACCTTATGTCCTTCCCACAAGCAGCCCCGCATGGTG - 24600
- L T F V E R A T T L C P S H K Q P R M V
- * L L W K G L P P Y V L P T S S P A W C
- D F C G K G Y H L M S F P Q A A P H G V
24601 - TTGTCTTCTACATGTACGTATGTGCCATCCAGGAGAGGAACCTCACCACAGCGCCAG - 24660
- L S S Y M S R M C H P R R G T S P Q R Q
- C L P T C H V C A I P G E E L H H S A S
- V F L H V T Y V P S Q E R N F T T A P A
24661 - CAATTTGTCTGAAGGCAAAGCATACTTCCCTCGTGAAGGTGTTTTTGTGTTTAAATGGCA - 24720
- Q F V M K A K H T S L V K V F L C L M A
- N L S * R Q S I L P S * R C F C V * W H
- I C H E G K A Y F P R E G V F V F N G T
24721 - CTTCTTGGTTTATTACACAGAGGAACCTTCTTTCTCCACAAATAATTACTACAGACAATA - 24780
- L L G L L H R G T S F L H K * L L Q T I
- F L V Y Y T E E L L F S T N N Y Y R Q Y
- S W F I T Q R N F F S P Q I I T T D N T
24781 - CATTTGTCTCAGGAAATTGTGATGTCGTTATTTGGCATCATTAAACAACAGTTTATGATC - 24840
- H L S Q E I V M S L L A S L T T Q F M I
- I C L R K L * C R Y W H H * Q H S L * S
- F V S G N C D V V I G I I N N T V Y D P
24841 - CTCTGCAACCTGAGCTTGACTCATTCAAAGAAGAGCTGGACAAGTACTTCAAAAATCATA - 24900
- L C N L S L T H S K K S W T S T S K I I
- S A T * A * L I Q R R A G Q V L Q K S Y
- L Q P E L D S F K E E L D K Y F K N H T
24901 - CATCACCAGATGTTGATCTTGGCGACATTTCAGGCATTAACGCTTCTGTCGTCAACATTC - 24960
- H H Q M L I L A T F Q A L T L L S S T F
- I T R C * S W R H F R H * R F C R Q H S
- S P D V D L G D I S G I N A S V V N I Q
24961 - AAAAAGAAATTGACCGCTCAATGAGGTCGCTAAAAATTAAATGAATCACTCATTGACC - 25020
- K K K L T A S M R S L K I * M N H S L T
- K R N * P P Q * G R * K F K * I T H * P
- K E I D R L N E V A K N L N E S L I D L
25021 - TTCAAGAATTGGGAAATATGAGCAATATATTAAATGGCCTTGGTATGTTTGGCTCGGCT - 25080
- F K N W E N M S N I L N G L G M F G S A
- S R I G K I * A I Y * M A L V C L A R L
- Q E L G K Y E Q Y I K W P W Y V W L G F
25081 - TCATTGCTGGACTAATTGCCATCGTCATGGTTACAATCTTGCTTTGTTGCATGACTAGTT - 25140
- S L L D * L P S S W L Q S C F V A * L V
- H C W T N C H R H G Y N L A L L H D * L
- I A G L I A I V M V T I L L C C M T S C
25141 - GTTCAGTTGCCTCAAGGGTGCATGCTCTTGTGGTTCTTGCTGCAAGTTTGATGAGGATG - 25200
- V A V A S R V H A L V V L A A S L M R M
- L Q L P Q G C M L L W F L L Q V * * G *
- C S C L K G A C S C G S C C K F D E D D

FIG. 4 Cont'd

25201 - ACTCTGAGCCAGTTCTCAAGGGTGTCAAATTACATTACACATAAACGAACTTATGGATTT - 25260
- T L S Q F S R V S N Y I T H K R T Y G F
- L * A S S Q G C Q I T L H I N E L M D L
- S E P V L K G V K L H Y T * T N L W I C
25261 - GTTTATGAGATTTTTACTCTTGGATCAATTACTGCACAGCCAGTAAAAATTGACAATGC - 25320
- V Y E I F Y S W I N Y C T A S K N * Q C
- F M R F F T L G S I T A Q P V K I D N A
- L * D F L L L D Q L L H S Q * K L T M L
25321 - TTCTCTGCAAGTACTGTTTCATGCTACAGCAACGATACCGCTACAAGCCTCACTCCCTTT - 25380
- F S C K Y C S C Y S N D T A T S L T P F
- S P A S T V H A T A T I P L Q A S L P F
- L L Q V L F M L Q Q R Y R Y K P H S L S
25381 - CGGATGGCTTGTATTGGCGTTGCATTCTTGCTGTTTTTCAGAGCGCTACCAAAATAAT - 25440
- R M A C Y W R C I S C C F S E R Y Q N N
- G W L V I G V A F L A V F Q S A T K I I
- D G L L L A L H F L L F F R A L P K * L
25441 - TGGCTCAATAAAGATGGCAGCTAGCCCTTTATAAGGGCTTCCAGTTCATTGCAATTT - 25500
- C A Q * K M A A S P L * G L P V H L Q F
- A L N K R W Q L A L Y K G F Q F I C N L
- R S I K D G S * P F I R A S S S F A I Y
25501 - ACTGCTGCTATTTGTTACCATCTATTCACATCTTTTGCTTGTGCTGCAGGTATGGAGGC - 25560
- T A A I C Y H L F T S F A C R C R Y G G
- L L L F V T I Y S H L L L V A A G M E A
- C C Y L L P S I H I F C L S L Q V W R R
25561 - GCAATTTTTGTACCTCTATGCCTTGATATATTTTCTACAATGCATCAACGCATGTAGAAT - 25620
- A I F V P L C L D I F S T M H Q R M * N
- Q F L Y L Y A L I Y F L Q C I N A C R I
- N F C T S M P * Y I F Y N A S T H V E L
25621 - TATTATGAGATGTTGGCTTTGTTGGAAGTGCAATCCAAGAACCCATTACTTTATGATGC - 25680
- Y Y E M L A L L E V Q I Q E P I T L * C
- I M R C W L C W K C K S K N P L L Y D A
- L * D V G F V G S A N P R T H Y F M M P
25681 - CAACTACTTTGTTTGCTGGCACACACATAACTATGACTACTGTATACCATATAACAGTGT - 25740
- Q L L C L L A H T * L * L L Y T I * Q C
- N Y F V C W H T H N Y D Y C I P Y N S V
- T T L F A G T H I T M T T V Y H I T V S
25741 - CACAGATACAATTGTCGTTACTGAAGGTGACGGCATTTC AACACCAAAACTCAAAGAAGA - 25800
- H R Y N C R Y * R * R H F N T K T Q R R
- T D T I V V T E G D G I S T P K L K E D
- Q I Q L S L L K V T A F Q H Q N S K K T
25801 - CTACCAAAITGGTGGTTATTCTGAGGATAGGCCTCAGGTGTTAAAGACTATGTCGTTGT - 25860
- L P N W W L F * G * A L R C * R L C R C
- Y Q I G G Y S E D R H S G V K D Y V V V
- T K L V V I L R I G T Q V L K T M S L Y
25861 - ACATGGCTATTTACCGAAGTTTACTACCAGCTTGAGTCTACACAAATTACTACAGACAC - 25920
- T W L F H R S L L P A * V Y T N Y Y R H
- H G Y F T E V Y Y Q L E S T Q I T T D T
- M A I S P K F T T S L S L H K L L Q T L
25921 - TGGTATTGAAAATGCTACATTCTTCATCTTTAACAAGCTTGTTAAAGACCCACCGAATGT - 25980
- W Y * K C Y I L H L * Q A C * R P T E C
- G I E N A T F F I F N K L V K D P P N V
- V L K M L H S S S L T S L L K T H R M C
25981 - GCAAATACACAAATCGACGGCTCTCAGGAGTTGCTAATCCAGCAATGGATCCAATTTA - 26040
- A N T H N R R L F R S C * S S N G S N L
- Q I H T I D G S S G V A N P A M D P I Y
- K Y T Q S T A L Q E L L I Q Q W I Q F M
26041 - TGATGAGCCGACGACGACTACTAGCCTGCTTTGTAAGCACAAGAAAGTGAGTACGAAC - 26100
- * * A D D D Y * R A F V S T R K * V R T
- D E P T T T T S V P L * A Q E S E Y E L
- M S R R R L L A C L C K H K V S T N L

FIG. 4 Cont'd

26101 - TATGTACTCATTCTGTTTCGGAAGAAACAGGTACGTTAATAGTTAATAGCGTACTTCTTTT - 26160
- Y V L I R F G R N R Y V N S * * R T S F
- M Y S F V S E E T G T L I V N S V L L F
- C T H S F R K K Q V R * * L I A Y F F F
26161 - TCTTGCTTTTCGTGGTATTCTTGCTAGTCACACTAGCCATCCTTACTGCGCTTCGATTGTG - 26220
- S C F R G I L A S H T S H P Y C A S I V
- L A F V V F L L V T L A I L T A L R L C
- L L S W Y S C * S H * P S L L R F D C V
26221 - TGCCTACTGCTGCAATATTGTTAACGTGAGTTTAGTAAACCAACGGTTTACGTCTACTC - 26280
- C V L L Q Y C * R E F S K T N G L R L L
- A Y C C N I V N V S L V K P T V Y V Y S
- R T A A I L L T * V * * N Q R F T S T R
26281 - GCGTGTTAAAAATCTGAACCTCTTCTGAAGGAGTTCTGATCTTCTGGTCTAAACGAATA - 26340
- A C * K S E L F * R S S * S S G L N E L
- R V K N L N S S E G V P D L L V * T N *
- V L K I * T L L K E F L I F W S K R T N
26341 - ACTATTATTATTATTCTGTTTGAACCTTTAACATTGCTTATCATGGCAGACAACGGTACT - 26400
- T I I I I L F G T L T L L I M A D N G T
- L L L L F C L E L * H C L S W Q T T V L
- Y Y Y Y S V W N F N I A Y H G R Q R Y Y
26401 - ATTACCGTTGAGGAGCTTAAACAACCTCTGGAACAATGGAACCTAGTAATAGGTTTCTTA - 26460
- I T V E E L K Q L L E Q W N L V I G F L
- L P L R S L N N S W N N G T * * * V S Y
- Y R * G A * T T P G T M E P S N R F P I
26461 - TTCCTAGCCTGGATTATGTTACTACAATTTGCTATTCTAATCGGAACAGGTTTTTGTAC - 26520
- F L A W I M L L Q F A Y S N R N R F L Y
- S * P G L C Y Y N L P I L I G T G F C T
- P S L D Y V T T I C L F * S E Q V F V H
26521 - ATAATAAGCTTGTTTTCTCTGGCTCTTGTTGGCCAGTAACACTTGCTTGTTTTGTGCTT - 26580
- I I K L V F L W L L W P V T L A C F V L
- * * S L F S S G S C G Q * H L L V L C L
- N K A C F P L A L V A S N T C L F C A C
26581 - GCTGCTGTCTACAGAATTAATTGGGTGACTGGCGGGATTGCGATTGCAATGGCTTGTATT - 26640
- A A V Y R I N W V T G G I A I A M A C I
- L L S T E L I G * L A G L R L Q W L V L
- C C L Q N * L G D W R D C D C N G L Y C
26641 - GTAGGCTTGATGTGGCTTAGCTACTTCGTTGCTTCTTCAGGCTGTTTGTCTCGTACCCGC - 26700
- V G L M W L S Y F V A S F R L F A R T R
- * A * C G L A T S L L P S G C L L V P A
- R L D V A * L L R C F L Q A V C S Y P L
26701 - TCAATGTGGTCATTCAACCCAGAAACAAACATTCTTCTCAATGTGCCTCTCCGGGGGACA - 26760
- S M W S F N P E T N I L L N V P L R G T
- Q C G H S T Q K Q T F F S M C L S G G Q
- N V V I Q P R N K H S S Q C A S P G D N
26761 - ATGTGACCAGACCGCTCATGGAAAGTGAACCTTGTCATTGGTGTGTGATCATTCTGTTG - 26820
- I V T R P L M E S E L V I G A V I I R G
- L * P D R S W K V N L S L V L * S F V V
- C D Q T A H G K * T C H W C C D H S W S
26821 - CACTTGCGAATGGCCGACACTCCCTAGGGCGCTGTGACATTAAGGACCTGCCAAAAGAG - 26880
- H L R M A G H S L G R C D I K D L P K E
- T C E W P D T P * G A V T L R T C Q K R
- L A N G R T L P R A L * H * G P A K R D
26881 - ATCACTGTGGCTACATCAGAACGCTTTCTTATTACAAATTAGGAGCGTCGACGCTGTA - 26940
- I T V A T S R T L S Y Y K L G A S Q R V
- S L W L H H E R F L I T N * E R R S V *
- H C G Y I T N A F L L Q I R S V A A C R
26941 - GGCCTGATTGAGTTTGTGCTGCATACACCGCTACCGTATTGAAACTATAAATTAAAT - 27000
- G T D S G F A A Y N R Y R I G N Y K L N
- A L I Q V L L H T T A T V L E T I N * I
- H * F R F C C I Q P L P Y W K L * I K Y

FIG. 4 Cont'd

27001 - ACAGACCACGCCGGTAGCAACGACAATATTGCTTTGCTAGTACAGTAAGTGACAACAGAT - 27060
- T D H A G S N D N I A L L V Q * V T T D
- Q T T P V A T T I L L C * Y S K * Q Q M
- R P R R * Q R Q Y C F A S T V S D N R C
27061 - GTTTCATCTTGTTGACTTCCAGGTTACAATAGCAGAGATATTGATTATCATTATGAGGAC - 27120
- V S S C * L P G Y N S R D I D Y H Y E D
- F H L V D F Q V T I A E I L I I I M R T
- F I L L T S R L Q * Q R Y * L S L * G L
27121 - TTTCAGGATTGCTATTTGGAATCTTGACGTTATAATAAGTTCAATAGTGAGACAATTATT - 27180
- F Q D C Y L E S * R Y N K F N S E T I I
- F R I A I W N L D V I I S S I V R Q L F
- S G L L F G I L T L * * V Q * * D N Y L
27181 - TAAGCCTCTAACTAAGAAGATTATTCGGAGTTAGATGATGAAGAACCTATGGAGTTAGA - 27240
- * A S S N * E E L F G V R * * R T Y G V R
- K P L T K K N Y S E L D D E E P M E L D
- S L * L R R I I R S * M M K N L W S * I
27241 - TTATCCATAAAACGAACATGAAAATTATTCTCTCTGACATTGATTGTATTACATCTT - 27300
- L S I K R T * K L F S S * H * L Y L H L
- Y P * N E H E N Y S L P D I D C I Y I L
- I H K T N M K I I L F L T L I V F T S C
27301 - GCGAGCTATATCACTATCAGGAGTGTGTAGAGGTACGACTGTACTACTAAAAGAACCTT - 27360
- A S Y I T I R S V L E V R L Y Y * K N L
- R A I S L S G V C * R Y D C T T K R T L
- E L Y H Y Q E C V R G T T V L L K E P C
27361 - GCCCATCAGGAACATACGAGGGCAATTCACCATTTACCTCTTGCTGACAATAAATTG - 27420
- A H Q E H T R A I H H F T L L L T I N L
- P I R N I R G Q F T I S P S C * Q * I C
- P S G T Y E G N S P F H P L A D N K F A
27421 - CACTAACTTGCACTAGCACACACTTTGCTTTTGCTGTGCTGACGGTACTCGACATACCT - 27480
- H * L A L A H T L L L L V L T V L D I P
- T N L H * H T L C F C L C * R Y S T Y L
- L T C T S T H F A F A C A D G T R H T Y
27481 - ATCAGCTGCGTGCAAGATCAGTTTCACCAAACCTTTTCATCAGACAAGAGGAGGTTCAAC - 27540
- I S C V Q D Q F H Q N F S S D K R R F N
- S A A C K I S F T K T F H Q T R G G S T
- Q L R A R S V S P K L F I R Q E E V Q Q
27541 - AAGAGCTCTACTCGCCACTTTTTCTCATTTGCTGCTCTAGTATTTTAACTTTGCT - 27600
- K S S T R H F F S L L L * Y F * Y F A
- R A L L A T F S H C C C S S I F N T L L
- E L Y S P L F L I V A A L V F L I L C F
27601 - TCACCATTAAGAGAAAGACAGAAATGAATGAGCTCACTTAATTGACTTCTATTTGTGCTT - 27660
- S P L R E R Q N E * A H F N * L L F V L
- H H * E K D R M N E L T L I D F Y L C F
- T I K R K T E * M S S L * L T S I C A F
27661 - TTTAGCCTTTCTGCTATTCTGTTTAAATAAGCTTATTATATTTGGTTTTCCTCGA - 27720
- F S L S A I P C F N N A Y Y I L V F T R
- L A F L L F L V L I M L I I F W F S L E
- * P F C Y S L F * * C L L Y F G F H S K
27721 - AATCCAGGATCTAGAAGAACCTTGTAACCAAGTCTAAACGAACATGAAACTTCTCATTGT - 27780
- N P G S R R T L Y Q S L N E H E T S H C
- I Q D L E E P C T K V * T N M K L L I V
- S R I * K N L V P K S K R T * N F S L F
27781 - TTTGACTTGTATTTCTCTATGCAGTTGCATACGCACTGTAGTACAGCGCTGTGCATCTAA - 27840
- F D L Y F S M Q L H T H C S T A L C I *
- L T C I S L C S C I R T V V Q R C A S N
- * L V F L Y A V A Y A L * Y S A V H L I
27841 - TAAACCTCATGTGCTTGAAGATCCTTGAAGGTACAACACTAGGGTAATACTTATAGCA - 27900
- * T S C A * R S L * G T T L G V I L I A
- K P H V L E D P C K V Q H * G * Y L * H
- N L M C L K I L V R Y N T R G N T Y S T

FIG. 4 Cont'd

27901 - CTGCTTGGCTTTGTGCTCTAGGAAAGGTTTACCTTTTCATAGATGGCACACTATGGTTC - 27960
- L L G F V L * E R F Y L F I D G T L W F
- C L A L C S R K G F T F S * M A H Y G S
- A W L C A L G K V L P F H R W H T M V Q
27961 - AAACATGCACACCTAATGTTACTATCAACTGTCAAGATCCAGCTGGTGGTGGCTTATAG - 28020
- K H A H L M L L S T V K I Q L V V R L *
- N M H T * C Y Y Q L S R S S W W C A Y S
- T C T P N V T I N C Q D P A G G A L I A
28021 - CTAGGTGTTGGTACCTTCATGAAGGTCACCAAAGTCTGCATTAGAGACGTACTTGTG - 28080
- L G V G T F M K V T K L L H L E T Y L L
- * V L V P S * R S P N C C I * R R T C C
- R C W Y L H E G H Q T A A F R D V L V V
28081 - TTTTAAATAAACGAACAAATTAATGTCTGATAATGGACCCCAATCAACCAACGTAGT - 28140
- F * I N E Q I K M S D N G P Q S N Q R S
- F K * T N K L K C L I M D P N Q T N V V
- L N K R T N * N V * * W T P I K P T * C
28141 - GCCCCCGCATTACATTTGGTGGACCCACAGATTCAACTGACAATAACCAAGATGGAGGA - 28200
- A P R I T F G G P T D S T D N N Q N G G
- P P A L H L V D P Q I Q L T I T R M E D
- P P H Y I W W T H R F N * Q * P E W R T
28201 - CGCAATGGGGCAAGGCCAAAACAGCGCCGACCCCAAGGTTTACCCAATAATACTGCGTCT - 28260
- R N G A R P K Q R R P Q G L P N N T A S
- A M G Q G Q N S A D P K V Y P I I L R L
- Q W G K A K T A P T P R F T Q * Y C V L
28261 - TGGTTCACAGCTCTCACTCAGCATGGCAAGGAGGAAGTCTAGATTCCCTCGAGGCCAGGGC - 28320
- W F T A L T Q H G K E E L R F P R G Q G
- G S Q L S L S M A R R N L D S L E A R A
- V H S S H S A W Q G G T * I P S R P G R
28321 - GTTCCAATCAACACCAATAGTGGTCCAGATGACCAAATTTGGCTACTACCGAAGAGCTACC - 28380
- V P I N T N S G P D D Q I G Y Y R R A T
- F Q S T P I V V Q M T K L A T T E E L P
- S N Q H Q * W S R * P N W L L P K S Y P
28381 - CGACGAGTTCGTGGTGGTGACGGCAAAATGAAAGAGCTCAGCCCCAGATGGTACTTCTAT - 28440
- R R V R G G D G K M K E L S P R W Y F Y
- D E F V V V T A K * K S S A P D G T S I
- T S S W W * R Q N E R A Q P Q M V L L L
28441 - TACCTAGGAAGTGGCCAGAGCTTCACTTCCCTACGGCGCTAACAAAGAAGGCATCGTA - 28500
- Y L G T G P E A S L P Y G A N K E G I V
- T * E L A Q K L H F P T A L T K K A S Y
- P R N W P R S F T S L R R * Q R R H R M
28501 - TGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCACATTGGCACCCGCAATCCT - 28560
- W V A T E G A L N T P K D H I G T R N P
- G L Q L R E P * I H P K T T L A P A I L
- G C N * G S L E Y T Q R P H W H P Q S *
28561 - AATAACAATGCTGCCACCGTGCTACAATTCCTCAAGGAACAACATTGCCAAAAGGCTTC - 28620
- N N N A A T V L Q L P Q G T T L P K G F
- I T M L P P C Y N F L K E Q H C Q K A S
- * Q C C H R A T T S S R N N I A K R L L
28621 - TACGCAGAGGGGAAGCAGAGGCGGAGTCAAGCCTCTTCTCGCTCCTCATCAGTAGTCGC - 28680
- Y A E G S R G G S Q A S S R S S S R S R
- T Q R E A E A A V K P L L A P H H V V A
- R R G K Q R R Q S S L F S L L I T * S R
28681 - GGTAATTCAGAAATTCACCTCTGGCAGCAGTAGGGGAAATTCCTGCTCGAATGGCT - 28740
- G N S R N S T P G S S R G N S P A R M A
- V I Q E I Q L L A A V G E I L L L E W L
- * F K K F N S W Q Q * G K F S C S N G *
28741 - AGCGGAGGTGGTGAAACTGCCCTCGCGCTATTGTGCTAGACAGATTGAACCAGCTTGAG - 28800
- S G G E T A L A L L L L D R L N Q L E
- A E V V K L P S R Y C C * T D * T S L R
- R R W * N C P R A I A A R Q I E P A * E

FIG. 4 Cont'd

28801 - AGCAAAGTTTCTGGTAAAGGCCAACAACAACAGGCCAAACTGTCTACTAAGAAATCTGCT - 28860
- S K V S G K G Q Q Q Q G Q T V T K K S A
- A K F L V K A N N N K A K L S L R N L L
- Q S F W * R P T T T R P N C H * E I C C
28861 - GCTGAGGCATCTAAAAAGCCTCGCCAAAAACGTACTGCCACAAAACAGTACAACGTCCT - 28920
- A E A S K K P R Q K R T A T K Q Y N V T
- L R H L K S L A K N V L P Q N S T T S L
- * G I * K A S P K T Y C H K T V Q R H S
28921 - CAAGCATTGGGAGACGTGGTCCAGAACAACCCAAAGGAAATTCGGGGACCAAGACCTA - 28980
- Q A F G R R G P E Q T Q G N F G D Q D L
- K H L G D V V Q N K P K E I S G T K T *
- S I W E T W S R T N P R K F R G P R P N
28981 - ATCAGACAAGGAAGTATTACAAACATTGGCCGCAAATTGCACAATTTGCTCCAAGTGCC - 29040
- I R Q G T D Y K H W P Q I A Q F A P S A
- S D K E L I T N I G R K L H N L L Q V X
- Q T R N * L Q T L A A N C T I C S K C X

29041 - TCTGCATTCTTTGGAATGTACGCATTGGCATGGAAGTCACACCTTCGGGAACATGGCTG - 29100
- S A F F G M S R I G M E V T P S G T W L
- L H S L E C H A L A W K S H L R E H G *
- C I L W N V T H W H G S H T F G N M A D
29101 - ACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACAATTCAAAGACAACGTCATA - 29160
- T Y H G A I K L D D K D P Q F K D N V I
- L I M E P L N W M T K I H N S K T T S Y
- L S W S H * I G * Q R S T I Q R Q R H T
29161 - CTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACCAACAGAGCCTAAAAAGGAC - 29220
- L L N K H I D A Y K T F P P T E P K K D
- C * T S T L T H T K H S H Q Q S L K R T
- A E Q A H * R I Q N I P T N R A * K G Q
29221 - AAAAAAGAAAGACTGATGAAGCTCAGCCTTTGCCGAGAGACAAAAGAAGCAGCCCACT - 29280
- K K K K T D E A Q P L P Q R Q K K Q P T
- K R K R L M K L S L C R R D K R S S P L
- K E K D * * S S A F A A E T K E A A H C
29281 - GTGACTCTTCTTCTGCGGCTGACATGGATGATTCTCCAGACAACCTTCAAATTCATG - 29340
- V T L L P A A D M D D F S R Q L Q N S M
- * L F F L R L T W M I S P D N F K I P *
- D S S S C G * H G * F L Q T T S K F H E
29341 - AGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATGACCACACAAGGCAGA - 29400
- S G A S A D S T Q A * T L M M T T Q G R
- V E L L L I Q L R H K H S * * P H K A D
- W S F C * F N S G I N T H D D H T R Q M
29401 - TGGGCTATGTAAACGTTTTCGCAATTCCGTTTACGATACATAGTCTACTCTGTGCAGAA - 29460
- W A M * T F S Q F R L R Y I V Y S C A E
- G L C K R F R N S V Y D T * S T L V Q N
- G Y V N V F A I P P T I H S L L L C R M
29461 - TGAATTCTCGTAACTAAACAGCACAAGTAGGTTTAGTTAACTTTAATCTCACATAGCAAT - 29520
- * I L V T K Q H K * V * L T L I S H S N
- E F S * L N S T S R F S * L * S H I A I
- N S R N * T A Q V G L V N F N L T * Q S
29521 - CTTTAATCAATGTGTAACATTAGGGAGGACTTGAAAGAGCCACCACATTTTCATCGAGGC - 29580
- L * S M C N I R E D L K E P P H F H R G
- F N Q C V T L G R T * K S H H I F I E A
- L I N V * H * G G L E R A T T F S S R P
29581 - CACGCGGAGTACGATCGAGGGTACAGTGAATAATGCTAGGGAGAGCTGCCTATATGGAAG - 29640
- H A E Y D R G Y S E * C * G E L P I W K
- T R S T I E G T V N N A R E S C L Y G R
- R G V R S R V Q * I M L G R A A Y M E E
29641 - AGCCCTAATGTGTAATAATTTTAGTAGTCTATCCCATGTGATTTAATAGCTTCT - 29700
- S P N V * N * F * * C Y P H V I L I A S
- A L M C K I N F S S A I P M * F * * L L

FIG. 4 Cont'd

- P * C V K L I L V V L S P C D F N S F L
29701 - TAGGAGAATGACAAAAAAAAAAAAAAAAAAAAAAAAA - 29736
- * E N D K K K K K K K K X
- R R M T K K K K K K K K X
- G E * Q K K K K K K K X

FIG. 4 Cont'd

1 - GATGGGTCCTTTTCGGTTGGTTGGAGCTAGAGAACATCTAGACAAGAGATTGCTTGAAA - 60
- D G S F S V G W S * R T S R Q E I C L K
- M G P F R L V G A R E H L D K R F A * N
- W V L F G W L E L E N I * T R D L L E I
61 - TTTTAGACACATCGACAGCGAGCCGACGTACGGATCACGTGGATGCGTCATATTTGTTAT - 120
- F * T H R Q R A D V R I T W M R H I C Y
- F R H I D S E P T Y G S R G C V I F V I
- L D T S T A S R R T D H V D A S Y L L L
121 - TATTTAAATGACAGCAACTGTTCTTTGCTCATTGAGCAGGGAGAAGACGTCTGACGAAT - 180
- Y L K * Q Q L F F A H * A G R R R L T N
- I * N D S N C S L L I E Q G E D V * R M
- F K M T A T V L C S L S R E K T S D E C
181 - GCCAAAGCAGGCACAACGTCAGCTAGTAGTCGTATGGATCCAAAGCAGGCCACACTGGC - 240
- A K A G T T S A S S R M D P K Q A H T G
- P K Q A Q R Q L V V V W I Q S R P T L A
- Q S R H N V S * * S Y G S K A G P H W L
241 - TTTCATTCTACCTCTCGGAACAAGAACCACAGTTGCTCTTTTGTGTGCAGGTTGAGTCA - 300
- F P F Y L S E Q E P Q L L F C V Q V E S
- F H S T S R N K N H S C S F V C R L S Q
- S I L P L G T R T T V A L L C A G * V K
301 - AACCGACAGGAAGTCCAATCTCTGCACGATCACGCACCGAAGCCCTGAGACACCTTCTC - 360
- N G Q E V Q S L H D H A P K P L R H L L
- T D R K S N L C T I T H R S P * D T F S
- R T G S P I S A R S R T E A P E T P S P
361 - CGGGATAGCCTCCGTGCACTTGTGGAGTTTACCCTGAACACCAGATCATCTCGACCTT - 420
- R D S L R A L V E F L P * T P D H L D L
- G I A S V H L W S F Y R E H Q I I S T F
- G * P P C T C G V F T V N T R S S R P F
421 - TTTCGCATGACGGGGTCGAACCTGTGCGGATACACAAGTAATTGCAAGACTACGAAT - 480
- F P H D G V E L V G I H K * F A R L R N
- F R M T G S N L S G Y T S N L Q D Y G I
- S A * R G R T C R D T Q V I C K T T E F
481 - TCGTGGTTAGTGCCGGTGTTCAGCAACTCGACCAACGTCTTTACCTGCCGTAAGTCATG - 540
- S W L V P V F Q Q L D Q R L Y L P * V M
- R G * C R C S S N S T N V F T C R K S C
- V V S A G V P A T R P T S L P A V S H A
541 - CCAGCATCGCCATATTGTGACCCTCATGACACGGGTGTACACCCGCTTTGGGGTTAACGT - 600
- P A S P Y C D P H E H G V H P L W G * R
- Q H R H I V T L M S T V Y T R F G V N V
- S I A I L * P S * A R C T P A L G L T Y
601 - ATGGCGTTACAAGAAGAAGCATTTGCCATTATTCCTCGGCCACCAGTATCGATACCG - 660
- M A L Q E E A F L P L F P R P P V S I P
- W R Y K K K H S C H Y S L G H Q Y R Y R
- G V T R R S I L A I I P S A T S I D T V
661 - TAGCTAGATTTCAGAATACTGAATCCACTGCTCGAACCGTGACTAGGGTAACTTCTAATA - 720
- * L D F R I L N P L L E P * L G * L L I
- S * I S E Y * I H C S N R D * G N F * Y
- A R F Q N T E S T A R T V T R V T S N T
721 - CTTGTTTTGACCTTGTGATTCTGACCGTACCACGTGAGGCACTTGAGTGAGCACTCGAG - 780
- L V L T L * F V P S P R E A L E * A L E
- L F * P C D S Y R H H V R H L S E H S S
- C F D L V I R T V T T * G T * V S T R V
781 - TTACCTCCACGTCACTGAGCGATACAGCTGTTGTTAAAGACACCGGGTCTACCCATGGGA - 840
- L P P R Q * A I Q L L L K T P G L P M G
- Y L H V S E R Y S C C * R H R V Y P W E
- T S T S V S D T A V V K D T G S T H G R
841 - GAACTAACGTAGTTTCTAAAAGAGCGTGCAGCGCCCGTTTCAGTTACACGTGAGAAAGGCTT - 900
- E L T * F L K E R A R P F S Y T * E R L
- N * R S F * K S V R A R S V T R E K G L
- T N V V S K R A C A P V Q L H V R K A C

FIG. 5

901 - GTTGAAC TAATGTAGCTCAGCTTCTCTCCACAGATGACGACGGCACTGGTACTCGTACTT - 960
- V E L M * L S F S P Q M T T A L V L V L
- L N * C S S A S L H R * R R H W Y S Y F
- * T N V A Q L L S T D D D G T G T R T L
961 - TAACGGACCAAGTGAAGTCTCGGAGACTATTCTCGATGCTCGTGGTCTGTGGGAAGCTTTAA - 1020
- * R T K * L A R L F S M L V V C G K L *
- N G P S D S R D Y S R C S W S V G S F N
- T D Q V T R E T I L D A R G L W E A L I
1021 - TTCTCACGGTCTTTAAACTGTGAAAGTTTCCCTTACGGGTTTCAAACACAAAGGAGAA - 1080
- F S R F F K L * K F P L T G F K H K G E
- S H G S L N C E S F P L R V S N T K E N
- L T V L * T V K V S P Y G F Q T Q R R I
1081 - TTGAGTTTTTCAGTTTCAGTAAGTTGGTGCACAACCTTTTCTTTTCTGACTCCCAAAGTAC - 1140
- L S F Q F Q * V G A Q L F F F * L P K Y
- * V F S F S K L V H N F S F S D S Q S T
- E F S V S V S W C T T F L F L T P K V P
1141 - CCCGCATATGCGAGACACATGGGACAACGTAGAGGTGCTCCTCACATTGTTATACGTGAAC - 1200
- P A Y A R H M G Q R R G V L T L L Y V N
- P H M R D T W D N V E V S S H C Y T * T
- R I C E T H G T T * R C P H I V I R E Q
1201 - AGATGGAAC TACTTTACATTAGTAACGCTACTTCAAAGTACCGTCTGCACGCTGAAAGAC - 1260
- R W N Y F T L V T L L Q S T V C T L K D
- D G T T L H * * R Y F K V P S A R * K T
- M E L L Y I S N A T S K Y R L H A E R L
1261 - TTTCGGTGAACACTTGTAAACACCGTGACTTTTAAATCAATAACTTCTGGATGATGTACA - 1320
- F R * T L V T P * L L N Q * L P G * C T
- F G E H L * H R D F * I N N F L D D V H
- S V N T C N T V T F K S I T S W M M Y T
1321 - CCCATGGATGGATGATTACGACATCACTTTTACGGTACAGGACGGACAGTTCTGGGTCTC - 1380
- P M D G * L R H H F Y G T G R T V L G L
- P W M D D Y D I T F T V Q D G Q F W V S
- H G W M I T T S L L R Y R T D S S G S L
1381 - TAACCTGGACTCGTATCACAACGCTAATAGTGTGGTGAGTTTGTAACTTTGAGCTGAG - 1440
- * P G L V S Q R L I V L V S L * L * A E
- N L D S Y H N V * * C W * V C N F E L R
- T W T R I T T S N S V G E F V T L S * G
1441 - GCGTTCCTCCATCCTGATCTACAAAACCTCCGACACACAAACGGATACAACCGACGATA - 1500
- A F P P S * S T K P P T H K R I Q P T I
- R S L H P D L Q N L R H T N G Y N R R Y
- V P S I L I Y K T S D T Q T D T T D D I
1501 - TTATTGCGACGGATGACCCAAGGAGCAGATCAGACTATAACCGAGTCCGGTATGACCG - 1560
- L F A R M T Q G A R S R L * P S P V * P
- Y S H G * P K E H D H D Y N R V R Y D R
- I R T D D P R S T I T T I T E S G M T V
1561 - TAATGACCACTGTTACACCTCTGGAAC TACTCTAGAGGAAC TCTATGACTCAGCACTT - 1620
- * * P L L H L W N L L L E E L Y D S A L
- N D H C Y T S G T Y S * R N S M T Q H L
- M T T V T P L E L T P R G T L * L S T C
1621 - GCACAATTGTAATTGTAACAACCGCTAAAAGTAAACTTACTTCTCCAACGGTAGTAAAC - 1680
- A Q L * L * Q P L K V N L L L Q R * * N
- H N C N C N N R * K * T Y F S N G S K T
- T I V I V T T A K S K L T S P T V V K P
1681 - CGTAGAAAGAGACGAAGATGTTACGGAAATAACTGTGATATTTCTCAGAACTAATGTTT - 1740
- R R K R R R C S R K * L * Y F S E L M F
- V E R D E D V H G E N N C D I S Q N * C S
- * K E T K M F T E I T V I F L R T N V Q
1741 - AGAAAGTTTGGTAACAACCTCAGGACGCCATTGATATTTCAATGTTCCCTTTCGGGCAT - 1800
- R K F W * Q L R T P L I F Q W F P F G H
- E S F G N N S G R H * Y F N G S L S G I
- K V L V T T Q D A I D I S M V P F R A F

FIG. 5 Cont'd

1801 - TTTCCACGAACCTTGTAACCTGTTGTCTCTAGTCAAAATTGTGGTGACACACCAAAAGGG - 1860
- F P R T L * P V V S S Q N C G D T P K G
- F H E P C N L L S L V K I V V T H Q K G
- S T N L V T C C L * S K L W * H T K R E
1861 - AGTGTCCGACGACCACAATAGTCTAGTTAAAAACGCGGTGTGAACACGTCGTTTGGTG - 1920
- S V R R P Q * S S * K R A C E L R R L V
- V S D D H N S L V K N A R V N Y V V V *
- C P T T T I V * L K T R V * T T S F G E
1921 - AGTTAAGGACTAAACGTTTCTCGTCGACAGTGGTATGAACACCATAAAGACTTGTTCAGT - 1980
- S * G L N V S R R Q W Y E L P * R L V S
- V K D * T F L V D S G M N Y H K D L S V
- L R T K R F S S T V V * T T I K T C Q *
1981 - AATGCAGAACAGCTGCGGTACCAATATGAAGTCTGGACGAGTGGTTGTACAGTAATAA - 2040
- N A E Q L R Y Q I * S L D E W L S Q * *
- M Q N S C G T K Y E V W T S G C H S N N
- C R T A A V P N M K S G R V V V T V I I
2041 - TACCGTATACATTGACCACCAGAACATGTTGTCTGAAGAGTCACCAACAGATTAGAAAAC - 2100
- Y R I H * P P E H V V * R V T N R L E N
- T V Y I D H Q N M L S E E S P T D * K T
- P Y T L T T R T C C L K S H Q Q I R K P
2101 - CCGTGATGACAACCTTTTGAGTCCGGATAGAACTTACCTAATCCGCTTGAATCACGT - 2160
- P * * Q L F E S G * K L T * L R F E S R
- R D D N F L S P D R N L P N S A L N H V
- V M T T F * V R I E T Y L T P L * I T S
2161 - CCTCAACTTAAAGAGTTCCTACGAACCCCTAAGAGTTTAAAGAGTAATGTCCACAAAAA - 2220
- P Q L K E F L R T L * E F K E * C P Q K
- L N L K S S Y E P S K S L K S N V H K N
- S T * R V P T N P L R V * R V M S T K T
2221 - CTGTAGCAGTCCCAAGTTTATGTCCAACGAAGTCTATTGTAGTTCCTAACACATTTTACG - 2280
- L * Q F P V Y V Q R S L L * F L T H F T
- C S S S Q F M S N E V Y C S S * H I L R
- V A V P S L C P T K S I V V P N T F Y E
2281 - AAGTAACACACAATGTTCGTCGAGCTTTACACGTAACAGTTCAGTGATAGCGACCG - 2340
- K * L Q Q L F R E L Y T * L V Q * * R P
- S N Y N N C S V S F T R N * F S D S D R
- V T T I V P * A L H V T S S V I A T A
2341 - CGTTTCAACGCTAGTGAGTTGAATCCACTTCAGAAGTAGCGAGTTTCGTTCCCTGAAATG - 2400
- R F N A S E L N P L Q K * R V S F P E M
- V S T L V S * I H F R S S E F R S L K W
- F Q R * * V E S T S E V A S F V P * N G
2401 - GCAGTCACATATGCACCGTTCTCGTCGACGTTGATGAGTACGGAGAATTCCGTGGTTTT - 2460
- A V T Y A P F L V D V D E Y G E F R G F
- Q S H M H R S S S T L M S T E N S V V F
- S H I C T V P R R R * * V R R I P W F S
2461 - CTTCAATTGAAAGAACTTCCACTAAGTGTACTGTGTATGAATGGAGACTCCTCCAACAA - 2520
- L H W K E L P L S V L C H E W R L L Q Q
- F I G K N F H * V Y C V M N G D S S N K
- S L E R T S T K C T V S * M E T P P T R
2521 - GAGTTCTTGCCACTTGAGCTTCGTGAGCTCTGCGGGCAACTATCGAAGTGTTCCTCGA - 2580
- E F L P L E L R E L C G Q L S K C L P R
- S S C H L S F V S S A G N Y R S V Y L D
- V L A T * A S * A L R A T I E V F T S I
2581 - TAGCAACCGTGTGGTCAGACACATTTACCGGAGTACGAGAATCTCTAATTCCTGTTTCTT - 2640
- * Q P C G Q T H L P E Y E N L * F L F L
- S N R V V R H I Y R S T R I S N S C F L
- A T V W S D T F T G V R E S L I P V S C
2641 - GTTATGACGCGTAACAGAGGACCAATGACCGATGTTTGTACAGAAAGCGAATTTTCCC - 2700
- V M T R N R G P N D R C L L Q K A N F P
- L * R V T E D Q M T D V C Y R K R I F P
- Y D A * Q R T K * P M F V T E S E F S P

FIG. 5 Cont'd

2701 - CCACGTGGTTAATTTCCACATTGGAAACCTCTTCTATGACAAACCCCTTCAAGTTCCAATG - 2760
- P R G * F P H W K P L L * Q T L Q V P M
- H V V N F H I G N L F Y D K P F K F Q C
- T W L I S T L E T S S M T N P S S S N V
2761 - TTCTTACACTCTTAGTGTAACCTCGAACTACTTGCACAACCTGTTTCACGAATTACTTTTC - 2820
- F L H S * C K L E L L A Q L F H E L L F
- S Y T L S V N S N Y L H N C F T N Y F S
- L T L L V * T R T T C T T V S R I T F H
2821 - ACGAGACAGATGTGACAACCTTAGGCCATGGCTTCAATGACTCAAACGTACACAACATCGT - 2880
- T R Q M * Q L R P W L Q * L K R T Q H R
- R D R C D N L G H G F N D S N V H N I V
- E T D V T T * A M A S M T Q T Y T T S S
2881 - CTCGACAACACTTCTGAAATGTTGGTCAAAGACTAGAGGAATGGTTGTACCCATACTA - 2940
- L R Q H F * N V G Q R L E E W L Y P * L
- S D N T S E M L V K D * R N G C T H N *
- P T T L L K C W S K T R G M V V P I T R
2941 - GACTACTACCTCACATCGATGTAAGATGAATAAACTACTACGACCACTTCTTTTGAAA - 3000
- E L L T S H R C K M N K L L R P L L L L
- N Y S P H I D V R * I N Y Y D H F F * K
- T T H L T S M * D E * T T T T T S F E K
3001 - AGTAGTGACATACATAACAAGGAAATGGGAGGTCTACTCCTTCTTCTCTGCTACGTCTC - 3060
- S S A Y I T R K M G G L L L L L L R L
- V V H T * Q G K W E V Y S F F S C Y V S
- * C I H N K E N G R S T P S S P A T S H
3061 - ACACTCCTTCTTCTTAACTACTTTGGACACTTGTACTCATGCCATGTCTCTACTAATA - 3120
- T L L L L * L L W T L V L M P C L L L I
- H S F F F N Y F G H L Y S C H V S Y * *
- T P S S L T T L D T C T H A M S P T N S
3121 - GTTCCAGAGGGAGACCTTAAACCACGGAGTCGACTTTGTCAAGCTCAACTCCTTCTTCTT - 3180
- V P E G D L K P R S R L C Q A Q L L L L
- F Q R E T L N H G V D F V K L N S F F F
- S R G R P * T T E S T L S S S S T P S S S
3181 - CTCCTTCTGACCGACCTACTATGATGACTCGTTAGTCTCTAACTCGGTCTTGGTCTTGG - 3240
- L L L T D L L * * L V S L * L G L G L G
- S F * P T Y Y D D S L V S N S V L V L D
- P S D R P T M M T R * S L T R S W S W M
3241 - TGTGGACTTCTTGGTCAATTAGTCAAATGACCAATAAATTTGAATGACTGTTACAACGG - 3300
- C G L L G Q L V K * P I N F E * L L Q R
- V D F L V N * S N D Q * I L N D C Y N G
- W T S W S I S Q M T N K F * M T V T T V
3301 - TAATTTACACAACCTGTAGCAATTCCTCCGTGTTTCACGATTAGGATACCACTAACATTTA - 3360
- * F T Q L * Q F L R V S R L G Y H * H L
- N L H N C S N S S V F H D * D T T N I Y
- I Y T T V A I P P C F T I R I P L T F T
3361 - CGACGATTGTATGTGGACTTTGTACCACCACCACATCGTCCACGTGAGTTGTTCCGTTGG - 3420
- R R L Y V D F V P P P H R P R E L F R W
- D D C M W T L Y H H H I V H V S C S V G
- T I V C G L C T T T T S S T * V V P L V
3421 - TTACCACGGTACGTTTTCTCTCACTACTAATGTAATTCGATTACCGGGAGAATGTCAT - 3480
- L P R Y V F L S L L M * F D L P G E C H
- Y H G T F S S H Y * C N S I Y R E N V I
- T T V R F P L T T N V I R F T G R M S S
3481 - CCTCCCAGAACAAACGAAAGACCTGTATTAGAACGATTCTTCACAGACGTACAACAACCT - 3540
- P P R T N E R P V L E R F F T D V Q Q P
- L P E Q T K D L Y * N D S S Q T Y N N L
- S Q N K R K T C I R T I L H R R T T T W
3541 - GGATTGGATTACGTCCTGAGGTGCGAAGAAATCCGTCGTATACTTTTAAAGTTA - 3600
- G L D L R P L L * V E E F R R I L L K L
- D W I Y V H S C R S K N S V V Y F * S *
- I G F T S T P V G R R I P S Y T F K V K

FIG. 5 Cont'd

3601 - AGTGTCTGTAGAAATGAACGTGGTAACAACAGTCGTCCGTATAAACCACGATTGGTGAA - 3660
- S V L * N E R G N N S R P Y K P R F G E
- V S C R M N V V T T V V R I N H D L V K
- C P V E * T W * Q Q S S V * T T I W * S
3661 - GTCAGAAATGTTACACGCACGTCTGCCAAGCATGTGTCCAAATATAACGTCAGTTACTG - 3720
- V R N V H T H V C Q A C V Q I * R Q L L
- S E M F T R T S A K H V S K Y N V S Y C
- Q K C S H A R L P S M C P N I T S V T V
3721 - TTTGAGAAATACTCGTCCAACAGTACCTAATAGAACTATTGGACTTCGGATCTCACCTT - 3780
- F R E I L V Q Q Y L I E L L D F G S H L
- F E K Y S S N S T * * N Y W T S D L T F
- S R N T R P T V P N R T I G L R I S P S
3781 - CGTGGATTGTCTCTCGTGGTTTGTGTCCTTCTAAGGTTTGGACTCCTCTTAGACAG - 3840
- R G F V L L G G L C L L R F * L L F R Q
- V D L F S S V V C V F * G F D S S L D S
- W I C S P R W F V S S K V L T P L * T A
3841 - CATGTCTTCGGACAGCTACACTTCGGTTTTTAATCCGGACGTAACACTCCAATGGTGT - 3900
- H V F G Q L H F G F * F R T * L L Q W C
- M S S D S Y T S V F N S G R N Y S N G V
- C L R T A T L R F L I P D V T T P M V L
3901 - TGTGACCTTCTTTGATTCAAAGAATGGTTATTCAATGAGAACAAACGACTATAGTTACCA - 3960
- C D L L * F K E W L F N E N K R L * L P
- V T F F D S K N G Y S M R T N D Y S Y H
- * P S L I Q R M V I Q * E Q T T I V T I
3961 - TTCGAAATGGTACTAAGAGTCTTGACGAATCTCCACTTCTATACAGAAAGGAAGTCTTC - 4020
- F E M V L R V L Y E S P L L Y R K E L F
- S K W Y * E S C T N L H F Y T E R N S S
- R N G T K S L V R I S T S I Q K G T L P
4021 - CTACGTGGAATGTACCATCCACTACAATAGTGATCACCCTATAGTGAACACAACATTAT - 4080
- L R G M Y H P L Q * * S P L * * T Q H Y
- Y V E C T I H Y N S D H H Y S E H N I M
- T W N V P S T T I V I T T I V N T T L W
4081 - GGGAGGTTTTTCCGACCACCGTGATGACTCTACGAGAGTCTCGAAACTTCTTTCACGGT - 4140
- G R F F R P P * * L Y E S S R N F F H G
- G G F S D H R D D S T R V L E T S F T V
- E V F P T T V M T L R E F S K L L S R S
4141 - CAACTACTCATATATTGGTGCATGGGACCTGTTCTCTACACGACCAATATGTGAAGTCTCT - 4200
- Q L L I Y W C M G P V P T R P I C E L L
- N Y S Y I G A W D L F L H D Q Y V N S F
- T T H I L V H G T T C S Y T T N M * T P S
4201 - CGATTCTGACGAGAATTCTTTACGTTTAGACGTAAAATACATGATGGAAGTCTTCGTGGA - 4260
- R F * R E F F T F R R K I H D G S L R G
- D S D E N S L R L D V K Y M M E V F V D
- I L T R I L Y V * T * N T * W K S S W I
4261 - TTACGATTCCCTCTCTAAGATCCTTGACATAGGACCTTAAACTCTCTTACGAACGAGTA - 4320
- L R F L L * D P * H R T L N S L Y E R V
- Y D S F S K I L D I G P * T L F T N E Y
- T I P S L R S L T * D L K L S L R T S T
4321 - CGACTTCTCTGTTCTTTAATTACGGATATACGTACCTACAATCTCGGTATTACCGTTGG - 4380
- R L L C S F N Y G Y T Y L Q S R Y Y R W
- D F S V L L I T D I R T Y N L G I T V G
- T S L F F * L R I Y V P T I S V L P L V
4381 - TAGGTTGCATTATATTTCTTAATTTAAGTTCTCCCGTAGCAACTGATACCACAGGCT - 4440
- * V A F I F P * F * V L P * Q L I P Q A
- R L H S Y F L N F K F S R S N * Y H R L
- G C I H I S L I L S S P V A T D T T G *
4441 - AAGAAGAAAATATGATCATTTCTCGGACATCGAAGATAATAATGCTTCGACTTGAGAGAT - 4500
- K K K I * S F L G H R R * * C F D L R D
- R R K Y D H F S D I E D N N A S T * E I
- E E N M I I S R T S K I I M L R L E R F

FIG. 5 Cont'd

4501 - TTACTCGGCGAACAGTGTGTACGGTTAACCAATACACTGTGTACCAAATTAGAACTTCTC - 4560
- L L G E Q C Y G * P I H C V P K L E L L
- Y S A N S V T V N Q Y T V Y Q N * N F S
- T R R T V L R L T N T L C T K I R T S P
4561 - CGACGCGGACATACGCAAGAGAATTTGAGGACGGCATCACAGTCATAGTAGTGGTCTA - 4620
- R R A T Y A R E F R G R H H S H S S G L
- D A R H T Q E N F E D G I T V I V V V Y
- T R D I R K R I S R T A S Q S * * W S T
4621 - CGACAATGATGTATATTACCTATGGAGTGAAGCAGTAGTTTCTGTAGACTCCTCGTGAAA - 4680
- R Q * C I L P M E * S S S F C R L L V K
- D N D V Y Y L W S E A V V S V D S S * N
- T M M Y I T Y G V K Q * F L * T P R E T
4681 - CATCTTTGTCAAAGAAACCGACCGAGAATGTCTCTAACCAGGATAAGTCTGTGCGCATGT - 4740
- H L C Q R N R P R M S L T R I S P V A C
- I F V K E T D R E C L * P G * V L S H V
- S L S K K P T E N V S N Q D K S C R M S
4741 - CTCAATCCACAACCTAAAGAATTTCGCCACCACTGTTTAAACATGGTGTGAGACCTCTCG - 4800
- L N P Q L K E F A P L F * H M V * D L S
- S I H N L K N S H H C F N T W C E T S R
- Q S T T * R I R T T V L T H G V R P L G
4801 - GGGCAGCTCAAAGTAGAACTGCCACTCCAAGAAAGTGAAGTGTGTTGATTTCTCAGAGAAT - 4860
- G Q L K V E L P L Q E S E L F D F S E N
- G S S K * N C H S K K V N C L I S Q R I
- A A Q S R T A T P R K * T V * F L R E *
4861 - AGGGACGCCCTCCAATTCTGATATTTTACAAGTGTGACACCTGTTGTGATTAGAGGTG - 4920
- R D A L Q F * Y F H K C * H L L * L E V
- G T P S N S D I F T S V D T C C D * R C
- G R P P I L I F S Q V L T P V V I R G V
4921 - TGTGTCGAACACCTATACAGATACTGTATACCTGTCGTCAAACCAGGTTGTATGAACCTA - 4980
- C V E H L Y R Y C I P V V K P G C M N L
- V S N T Y T D T V Y L S S N Q V V * T Y
- C R T P I Q I L Y T C R Q T R L Y E P T
4981 - CCACGACTACAATGTTTTTAATTTGGAGTACATTAGTACTCCCATTCTGAAAGAAACAT - 5040
- P R L Q C F * F G V H L V L P F * K K H
- H D Y N V F N L E Y I * Y S H S E R N M
- T T T M F L I W S T F S T P I L K E T *
5041 - GATGGATCACTACTGTGTGATGCATCACTTCGAAAGCTCATGATGGTATGAGAACTACTC - 5100
- D G S L L C D A S L R K L M M V * E L L
- M D H Y C V M H H F E S S * W Y E N Y S
- W I T T V * C I T S K A H D G M R T T L
5101 - TCAAAAGAACCATCCATGTACAGACGAAATTTGGTGTGTTTCTTTACCTTTAAAGGAGTT - 5160
- S K E P S M Y R R N L V C F F T F K G V
- Q K N H P C T D E I W C V S L P L K E F
- K R T I H V Q T K F G V F L Y L * R S S
5161 - CAACCACCAAATTGAAGTTAATTTACCGACTATTGTTAACAATAAACAGATCACAAAAT - 5220
- Q P P N * S * F T R L L L T I N R S Q N
- N H Q I E V N L P D Y C * Q * T D H K I
- T T K L K L I Y P T I V N N K Q I T K *
5221 - AATCGTGAAGTTGTCGAACCTTCAGTTTAAGTTACGTGGTTCGTGAAGTTCTCCGAATAATA - 5280
- N R E V V E L Q F K L R G R E V L R I I
- I V K L S N F S L S Y V V V K F S E * Y
- S * S C R T S V * V T W S * S S P N N I
5281 - TCTCGGGCAGCACTACGACGATTGAAAACACGTGAGTATGAGCGAATGTCATTATTT - 5340
- S R A R P L R R L K T R E Y E R M S L F
- L G H D H Y D D * K H V S M S E C H Y F
- S G T T T T T I E N T * V * A N V I I L
5341 - TGACAACCGCTCGAACCCTACAGTCTCTTTGATACTGGGTAGAAGATGTCGTACGATTA - 5400
- * Q P L E P L Q S L * Y W V E D V V R L
- D N R S N H Y S L F D T G * K M S Y D *
- T T A R T T T V S L I L G R R C R T I K

FIG. 5 Cont'd

5401 - AACCTTAGACGTTTCGCTCAAGAATTACACCACACATTGTAAACACCACTCTTTTGATGA - 5460
- N L R R F A Q E L H H T F V T P V F * *
- T L D V S L K N Y T T H L * H Q S F D D
- P * T F R S R I T P H I C N T S L L M M
5461 - TGGAAATTGCCCACATCTTCGACACTACATATACCCATGAGATAGAATACTATTAGAATTC - 5520
- W N C P H L R H Y I Y P * D R I L L E F
- G I A H I F D T T Y T H E I E Y Y * N S
- E L P T S S T L H I P M R * N T I R I L
5521 - TGTCCACAAAGGTAAGGTACACACACACCAGCACTACGATGTGTTATAGATCATGTTGTT - 5580
- C P Q R * G T H T P A L R C V I D H V V
- V H K G K V H T H Q H Y D V L * I M L F
- S T K V R Y T H T S T T M C Y R S C C S
5581 - CTCAGAAGAAAACAATACTACAGACGTTGGTGACCACTCATATTTAATGTCGTTCCATGT - 5640
- L R R K Q Y Y R R G G R L I F N V V P C
- S E E N N T T D V V D D S Y L M S F H V
- Q K K T I L Q T W W T T H I * C R S M *
5641 - AAGAATACACGCTTACTCATGTGACCACTAGTAGTCACACCAAGTAATGTGAGTATATTGA - 5700
- K N T R L L M * P L I V T P V M * V Y *
- R I H A Y S C D H * * S H Q * C E Y I D
- E Y T L T H V T I D S H T S N V S I L T
5701 - CGATTCTCTGGGAGATAGCATAACTGCTCGAGTGGAAATGTTTCTACAGTCTCATGTTT - 5760
- R F L W E I A * L P R V E C F Y S L M F
- D S S G R * H N C L E W N V S T V S C F
- I P L G D S I T A S' S G M F L Q S H V S
5761 - CCTGGTCACTGACTACAAAAGATGTTCTTTGTAGAATGTGATGTTGGTAGTTCGGACAC - 5820
- P G H * L Q K M F L C R M * C W * F G H
- L V T D Y K R C S F V E C D V G S S D T
- W S L T T K D V P L * N V M L V V R T Q
5821 - AGCATTTTGAGCTACCTCAATGAATGTGTCTCTAACTGGTTTAACTACCCATAATA - 5880
- S I F E L P Q * M C L * L G F N L P I I
- A Y L S Y L N E C V S N L V L T Y P * Y
- H I * A T S M N V S L T W F * P T H N I
5881 - TTTTCTTATTACGAATGATATGTCTCGTCCGATATCTGGAACATGGTTGAGTTGGTAAT - 5940
- F F L L R M I C L V G Y L E H G * V G N
- F S Y Y E * Y V S S D I W N M V E L V M
- F P I T N D M S R R I S G T W L S W * W
5941 - GGTTTACGCTCAAAACTATTAAAGTTTGAGTGTACAAGATTGTGTTTAAACCACTACTA - 6000
- G L R S K L L K F E C T R L C F K R L L
- V Y A Q N Y * S L S V Q D C V L N D Y *
- F T L K T I K V * V Y K I V F * T T T K
6001 - AATTTAGTTTACTGTCCGAAGTGTTCGGTCCGAAGTCTCTCGATAGACAGTGTGAAGAAG - 6060
- N L V Y C P K C F G R S A L D R Q C K K
- I * F T V R S V S V E V L S I D S V R R
- F S L L S E V F R S K C S R * T V * E G
6061 - GGTCTGAACCTTACCGCTACATCACCGATACTGATATCTGTGATAAGTCGCTCAAAGTTC - 6120
- G L N L P L H H R * L I S V I S R S K F
- V * T Y R Y I T D N * Y L * * V A Q S S
- S E L T A T S P I T D I C D K S L K V L
6121 - TTTCCACGATTTAATGACGTATTCGGTTAACAACCGTGTAATTGGTCCGATGTTGGTTC - 6180
- F P R F N D V F G * Q T V * L V R C W F
- F H D L M T Y S V N K P C N W S D V G S
- S T I * * R I R L T N R V I G P M L V L
6181 - TGTTGCAAGTTTGGTTTGTGAACCACAAATGCAACAGAAACCTCATGTTTCGGTCATCTA - 6240
- C C K F G L * T T N A T E T S C F G H L
- V A S L V C E P Q M Q Q K P H V S V I Y
- L Q V W F V N H K C N R N L M F R S S M
6241 - TGAAGTTTAAGTAAACTCAAGACCGTCATCTTCTGTGTGTTCTTACCTGTTAGAACGA - 6300
- * S L S K L Q D R H L L C V P Y L L E R
- E V * V N F K T V I F C V F L T C * N E
- K F K * T S R P S S S V C S L P V R T N

FIG. 5 Cont'd

6301 - ACACCTTTTCAGTTGTTGGGTGGAGACTTCTTCATCACCTTTTAGGATGGTATGCTCTCCTT - 6360
- T L S V V G W R L L H H L L G W Y V F L
- H F Q L L G G D F F I T F * D G M S S F
- T F S C W V E T S S S P F R M V C L P S
6361 - CAGTATCTCACACTGCACCTTTTGATGGCTTCAACATCCGTTACAGTATGAATTTGGTAGT - 6420
- Q Y L T L H F * W L Q H P L Q Y E F G S
- S I S H C T F D G F N I R Y S M N L V V
- V S H T A L L M A S T S V T V * I W * S
6421 - CTACTTCCACAATTTTCATTGTGTTCTCAATCCAGTACTCCTAGAATACCGACGAATACAC - 6480
- L L P Q Q F H C V L N P V L L E Y R R I H
- Y F H N F I V F S I Q Y S * N T D E Y T
- T S T I S L C S Q S S T P R I P T N T P
6481 - CTTTTGTGTTTCGTAATGGTAATCTTTGGATTACTCGAAAGTGATCGGAATCCAAATTTT - 6540
- L L C S * W * F F G L L E S D R N P N F
- F C V R N G N S L D Y S K V I G I Q I F
- F V F V M V I L W I T R K * S E S K F L
6541 - TGTTAACGGTGAGTACCATAACGACGTTAATTATCACAAGGAACCTCATTTTAAACCGA - 6600
- C * R * V P * R R * L S Q G T S F * N R
- V N G E Y H N D V N Y H K E P H F K T E
- L T V S T I T T L I I T R N L I L K P N
6601 - ATACAGTTTGGTAAGAATCTGTTTCGTCGTTAATGTTGTAGTTTAACGCGATTCTCTAAT - 6660
- I Q F G K N P V R R * C C S L T R F S N
- Y S L V R I L F V V N V V V * R D S L I
- T V W * E S C S S L M L * F N A I L * S
6661 - CGTGTGTCACACAAATGTTAATATACGGAATACACAAATGTAATAACAAGGTTAACACA - 6720
- R V A H K L L I Y G I H K C N N K V N T
- V L H T N C * Y T E Y T N V I T R L T H
- C C T Q I V N I R N T Q M * * Q G * H M
6721 - TGAAATGATTTTCATGGTTAAGATCTTAATCTCGAAGTGATGGATGTTGATAACGATTT - 6780
- * K * F S W L R S * S R S D G C * * R F
- E N D F H G * D L N L E V M D V D N D F
- K M I F M V K I L I S K * W M L I T I F
6781 - TTATCACAATTTCTCACAACGATTTAATACAAACCTACGGCCGTAATTAATACACTTCAGT - 6840
- L S Q F S Q R F N T N L R P * L I H F S
- Y H N S H N D L I Q T Y G R N * Y T S V
- I T I L T T I * Y K P T A V I N T L Q W
6841 - GGGTTTAAAGATTTAACAAGTGTTAGCGATACACCGATAACAACAATTCAAAACGAAT - 6900
- G F K R F N K C * R Y T D N N N S * T N
- G L K D L T S V S D T P I T T I H K R I
- V * K I * Q V L A I H R * Q Q F I N E S
6901 - CCAAGAGATTAGACATTGACGACGAAAACCATGAGAATAGATTAAACCCAGGAGGA - 6960
- P R D * T H * R R K P H E N R L K P R G
- Q E I R H I D D E N H M R I D * N H E E
- K R L D T L T T K T T * E * I K T T R K
6961 - AGAATAACATTACCGCAATCTCTTAACATAGAATTAAGCAGATTGCAATGATGATACCTA - 7020
- R I T L P Q S L N I E L S R L Q * * Y L
- E * H Y R N L L T * N * A D C N D D T *
- N N I T A I S * H R I K Q I A M M I P K
7021 - AAGACACTTCCAAGAAAAGGAACGTCGTAAACAAATTCACCTAATCTGAGGGAACCTAAGA - 7080
- K T L P R K G T S * T N S P N L R E L R
- R H F Q E K E R R K Q I H L I * G N * E
- D T S K K R N V V N K F T * S E G T K N
7081 - ATAGGTCGAGAACCTTGGTAAGTCCACTGCTAAAGTAGCATGTTTCGATCTGAACTGTTAA - 7140
- I G R E L W * V H C * S S M F D L N C *
- * V E N F G K S T A K V A C S I * T V K
- R S R T L V S P L K * H V R S E L L K
7141 - AATCCAGACCGCGACTCACCCAAAACCGTATATACAACAAGTGTTTTAAGAAAATAAAT - 7200
- N P D R R L T Q N R I Y N K C F K K I N
- I Q T G D S P K T V Y T T S V L R K * I
- S R P A T H P K P Y I Q Q V F * E N K *

FIG. 5 Cont'd

7201 - AATCCAGAAAGTCGATATTACGTCCACAAGAAACCGATAAAACGATCAGTAAAGTAGTCG - 7260
- N P E S R Y Y V H K K P I K R S V K * S
- I Q K V D I T S T R N R * N D Q * S S R
- S R K S I L R P Q E T D K T I S K V V V
7261 - TTAAGAACCGAGTACACCAAATAGTAATCATAACATGTTTACCGTGGGCAAAGACGTTAC - 7320
- L R T E Y T K * * S * H V Y R G Q R R Y
- * E P S T P N S N H N M F T V G K D V T
- K N R V H Q I V I I T C L P W A K T L P
7321 - CAATCCTACATGTAGAAGAAACGAAGAAAGATGATGTATACCTTCTCGATACAAGTATAG - 7380
- Q S Y M * K K R R K M M Y T F S I Q V *
- N P T C R R N E E R * C I P S R Y K Y S
- I L H V E E T K K D D V Y L L D T S I V
7381 - TACCTACCAACGTGGAGAAGCTGAACGTACTACACGATATTCCGCTTAGCACGGTGTGCG - 7440
- Y L P T W R S * T Y Y T I F A L A R C A
- T Y Q R G E A E R T T R Y S R * H G V R
- P T N V E K L N V L H D I R V S T V C A
7441 - CAACTCACATGTTGATAACAATTACCGTACTTCTCTAGAAAGATACAGATACGTTTACCT - 7500
- Q L T C * * Q L P Y F S R K I Q I R L P
- N S H V D N N Y R T S L E R Y R Y V Y L
- T H M L I T I T V L L * K D T D T F T S
7501 - CCGGCACCGAAGACGTTCTGAGTGTAAACCTTAACAGAGTTAACACTGTGTAAAACGTGA - 7560
- P A P K T F * V L T L T E L T L C K T *
- R H R R R S E C * P * Q S * H C V K R D
- G T E D V L S V N L N R V N T V * N V T
7561 - CCATCATGTAAGTAATCACTACTTCAACGAGCACTAAACAGTGAGGTCAAATTTTCTGGT - 7620
- P S C K * S L L Q R A L N S E V K F S G
- H H V S N H Y F N E H * T V R S N F L V
- I M * V I T T S T S T K Q * G Q I F W L
7621 - TAGTTGGGATGACTGGTCAGTCATATAACAACATATCACAACGACACTTTTACC CGCGC - 7680
- * L G * L V S S I * Q L S Q R H F L P R
- S W D D W S V A Y N N Y H N D T F Y R A
- V G M T G Q * H I T T I T T T L F T A R
7681 - GAAGTGGAGATGAAACTGTTCCGACCACTTTTCTGGATACTCTCTGTAGGAGAGAGGGTA - 7740
- E V E M K L F R P V F W I L S V G E R V
- K W R * N C S D Q F S G Y S L * E R G *
- S G D E T V P T S F L D T L C R R E G K
7741 - AAACAGTTAAATCTGTTAAACTCTCGATTGTTGTGATTTC AAGTGACGGATAATTACAG - 7800
- K Q L N L L N S R L L * F P S D G * L Q
- N S * I C * T L D C C D F Q V T D N Y S
- T V K S V K L S I V V I S K * R I I T V
7801 - TATCAAAAACCTACCGTTCAGGTTTACGCTGCTCAGACGAAGATT CAGACGAAGACACATG - 7860
- Y Q K L P F R F T L L R R R F R R R H M
- I K N Y R S G L R C S D E D S D E D T *
- S K T T V Q V Y A A Q T K I Q T K T H D
7861 - ATGTCAGTCGACTACCGGTTGGATAAGACAACGAACCTGGTTCGAGAACATAGTCTGCAA - 7920
- M S V D Y T V G * D N E L V R E H S L Q
- C Q S T T R L D K T N W F E N I V C N
- V S R L H G W I R Q R T G S R T * S A T
7921 - CCTCTATCATGACTTCAAAGGCAATTCTACAACTACGAATACAGCTGTGGAAGAGTCGT - 7980
- P L S * L Q R Q F Y K L R I Q L W K S R
- L Y H D F K G N S T N Y E Y S C G K V V
- S I M T S K A I L Q T T N T A V E K S L
7981 - TGAATAATCACAAGGATACCTTTTGAATCCGTGAACAACGATGTCGAGTGTGCTCAAT - 8040
- * K S Q G Y L F E F R E Q R C R V S L N
- E N H K D T F L N S V N N D V E C R S I
- K I T R I P F * I P * T T M S S V A Q S
8041 - CGTTTCCCACATCGAAATCTACCACAGGAAGATGTAAGCACAGTCGACGGGCTGTCCA - 8100
- R F P H R N L P Q E R C K H S R R A V P
- V S H I E I Y H R K D V S T V D G L F H
- F P T S K S T T G K M * A Q S T G C S T

FIG. 5 Cont'd

8101 - CAACAACATATGGCTACAACGTGTTTCTACAATAACTTACAGAGTTTGAAAGTGTAGTG - 8160
- Q Q L W L Q L C F L Q * L T E F E S V V
- N N Y G Y N C V S Y N N L Q S L K V * *
- T T M A T T V F P T I T Y R V * K C S E
8161 - AGACTGAATCTTCACTGTCCACTGTCAACATTGTTAAAGTACGAGTGGATATTATCCAA - 8220
- R L N L H C P L S T L L K Y E W I L F Q
- D * I F T V H C Q H C * S T S G Y Y S N
- T E S S L S T V N I V K V R V D I I P T
8221 - CTTTGTACTGCGGGTCTCTAGAACCGGTACATAACTGACATTACGTTCCGTATAGTTA - 8280
- L L Y C G S L E P R T * L T L R S V * L
- F C T A G L * N R V H N * H Y V P Y S Y
- F V L R V S R T A Y I T D I T F R I V T
8281 - CGGGTTTCATCGTTTTCAGTGTACAAAGTGAGTAGACCTTACATTCTCTGATGTACAGA - 8340
- R V H R F S V L Q S E * T L H F L M Y R
- G F I V F Q C Y K V S R P Y I F * C T E
- G S S F F S V T K * V D L T F S D V Q K
8341 - AATAGACTTGTGACGCATTGTTTAAAGCATCAGGACGTTCTTCTGTTGTATGGAAAA - 8400
- N R L V D A F V * A S R R F F L L Y G K
- I D L S T H L F K H H D G S S C C M E N
- * T C R R I C L S I T T V L L V V W K I
8401 - TCTGATTGAACACGATGTTGATCTGTCCAACAGTTACAGTATTGATGATTTAGAGTGAG - 8460
- S D * T R C * S V Q Q L Q Y * * F * S E
- L I E H D V D L S N S Y S I D D F R V S
- * L N T M L I C P T V T V L M I L E * V
8461 - TTCCCACCATTTCTAACAATCATGAACAAAATTGAATACGAATTCGGGTGTAATAACAG - 8520
- F P P F * Q S * T K F E Y E F R C N N T
- S H H S N N H E Q N L N T N S G V I T R
- P T I L T I M N K I * I R I P V * * H A
8521 - CAAGAACGCGTAACCAACAATATAGCAATACGGTCATGTATGTAACAGTTAGGTACTA - 8580
- Q E R R N Q T I * Q Y G H V C N S * V L
- K N D V T K Q Y S N T V M Y V T V R Y Y
- R T T * P N N I A I R S C M * Q L G T T
8581 - CCAATGTGTTTACTTTAGTAACCAATGTTTCGGTAAGTCCTACCACAGTGAGCACTGTAG - 8640
- P M C L L * * P M F R * V L P Q * A L *
- Q C V Y F S N Q C F G K S Y H S E H C S
- N V F T L V T N V S V S P T V S T V V
8641 - TAAAGATGACTACTAACAAAACGTTTATTGTACGACCAAACTGCGTACCAAAATCGGTC - 8700
- * R * L L T K R L F V R P K L R T K S V
- K D D Y * Q N V Y L Y D Q N C V P N R S
- K M T T N K T F I C T T K T A Y Q I G R
8701 - GCACCACCAAGTATGTTTACTGTTTTCGACGGGACATCATCGACGATAGTAATGTTCT - 8760
- A P P S M F L L F S T G H H R R * * C S
- H H Q V C F Y C F R R D I I D D S N V L
- T T K Y V F T V F D G T S S T I V M F S
8761 - CTCTAACCAAGTATCAGGACCGAATGGCCCATGACACGACTCTCGTTAGTTACCACTG - 8820
- L * P K Y H G P N G P * H D S R * L P L
- S N Q S I T D R M A H D T T L V S Y H *
- L T K V S R T E W P M T R L S L V T T E
8821 - AAGAACGTAAAGATGGAGCACAAAAATCAGCACACCGTTGTAAACGATGTGTGAAGG - 8880
- K N V K D G A Q K S R Q P L * T M C G R
- R T * K M E H K N H D N R C K R C V E G
- E R K R W S T K I T T T V V N D V W K V
8881 - TTTGAGTAACATATCACTAAAACGATGGAGACGAACGCAAGAACGAGTACATGT - 8940
- F E * L I S L K R W R R T Q E R R L T C
- L S N S Y H * N D G D E R K N D D S H V
- * V T H I T K T M E T N A R T T T H M L
8941 - TAAAAATTCCTACGATACCCGTTTGGACACGGTATAACAATACTGTGATTAAACGATCTC - 9000
- * K F L R Y P F G H G I T I L * L N D L
- K N S Y D T R L D T V * Q Y C D * T I S
- K I P T I P V W T R Y N N T V I K R S P

FIG. 5 Cont'd

9001 - CCAAGATAAAGAATATCACTCGAAGCAGGTCTGTGAGCAATACACGAATACCTACCAAGG - 9060
- P R * R I S L E A G L * A I H E Y L P R
- Q D K E Y H S K Q V C E Q Y T N T Y Q G
- K I K N I T R S R S V S N T R I P T K V
9061 - TAGTATGTCAAAGGATTGTGAATGGACCTCCCAAGACAATCTCATCATTGTTGAAAATA - 9120
- * Y V K G L * M D L P R Q S H H C * K L
- S M S K D C E W T S Q D N L I I V E N Y
- V C Q R I V N G P P K T I S S L L K T T
9121 - CGACTCATGACATCTGTACCATGTACGCTTTCCAGTCTTCATCCATAAACGGATAGATGG - 9180
- R L M T S V P C T L S S L H P * T D R W
- D S * H L Y H V R F P V F I H K R I D G
- T H D I C T M Y A F Q S S S I N G * M V
9181 - TCACCTTACCCAAGAATTATTACTCGTAATGTCTCGAGATAGTCCTCAAAGACACCA - 9240
- S P S T Q E L L L V M S R D S P Q K T P
- H H L P K N Y Y S * C L E I V L K R H H
- T I Y P R I I T R N V S R * S S K D T T
9241 - CAACTACGCTACTTAGAGTATCGATTGTAGAAAATGAGGAGAACACGTTGGACACCCACGA - 9300
- Q L R Y L E Y R L * K * G E H V G H P R
- N Y A T * S I D C R N E E N T L D T H E
- T T L R V S I V E M R R T R W T P T K
9301 - AATCTACACAGACGAAGTCATCAGCACCACCATATAACGGTATAACCACTGAACACGA - 9360
- N L H R R S H H R P P * * R Y N H * T R
- I Y T D E V I T D H H N N G I T T E H D
- S T Q T K S S P T T I I T V * P L N T T
9361 - CGGATGATGAAATACTTTAAGTCTGCACGAAAACCACTCATGTTGGTACAACAACGACGA - 9420
- R M M K Y F K S A R K P L M L V Q Q R R
- G * * N T L S L H E N H S C W Y N N D D
- D D E I L * V C T K T T H V G T T T I
9421 - TTACGTGAAACAAAACCTACAGAAAGTATGAGACAGACCGTGGTGAATGTGAAA - 9480
- L R E N K N Y R K * Y E T D R G R M S K
- Y V K T K T T E S D M R Q T V V E C R K
- T * K Q K L Q K V I * D R P W S N V E R
9481 - GACGGCCCTCAGATGAGTCAGAAAATGAACATGAAGTGTAAAGATAAAGTGGTTACTACAA - 9540
- D G P Q M S Q K M N M N C K I K W L L Q
- T A L R * V R K * T * T V R * S G Y Y K
- R P S D E S E N E H E L * D K V V T T K
9541 - AGTAAGAACCGAGTGGAAGTTACCAACGGTACAAAAGAGGATAACACGGAACCTAT - 9600
- S K N R V E V T K R Y K R G * H G K T Y
- V R T E W K L P N G T K E D N T E K P I
- * E P S G S Y Q T V Q K R I T R K N L L
9601 - TGTCGTTAGATACATAAGACATAAGAGACTTCGTGACGGTAACCAAGAAATTGTTGATA - 9660
- C R * I H K T * R D F V T V T K K L L I
- V V R Y I R H K E T S * R * P R N C * *
- S L D T * D I K R L R D G N Q E I V D R
9661 - GAATCCTTTTCTCAGTACAAATTACCTCAATGTAAATCATGGAAGCTCCTCCGACGAAAC - 9720
- E S F S Q Y K L P Q C K S W K L L R R N
- N P F L S T N Y L N V N H G S S S D E T
- I L F S V Q I T S M * I M E A P P T K H
9721 - ACATGGAAAAACGAGTTGTTCTTACATGGATTTTAACGCATCGCTCTGTGACAACGGT - 9780
- T W K N E L F L Y M D F N A S L C D N G
- H G K T S C S F T W I L T H R S V T T V
- M E K R V V P L H G F * R I A L * Q R *
9781 - GAATGTGTGATATTGTCCATAGAACGAGATATATTGTTTCATGTTTATAAAGTCACCTCGG - 9840
- E C V I L S I E R D I L F M F I K S P R
- N V S Y C P * N E I Y C S C S * S H L G
- M C H I V H R T R Y I V H V H K V T S E
9841 - AATCTATGATGGTCGATAGCACTTCGTGGAACGACGGTGAATCGTTTCCGAGATTACTG - 9900
- N L * W S I A L R R T T V N R F R D L L
- I Y D G R * H F V E R R * I V S E I Y *
- S M M V D S T S S N D G E S F P R F T E

FIG. 5 Cont'd

9901 - AAATCGTTGAGTCCACGACTACAAGAGATGGTTGGTGGTCTGTAGTTAGTGAAGACGA - 9960
- K S L S P R L Q E M V G G V C S * * R R
- N R * V H D Y K R W L V V S V V S E D D
- I V E S T T T R D G W W C L * L V K T T
9961 - CAAGACGTCTACCAAATCCTTTTACCGTAAGGGCAGTCCGTTTCAACTTCCCACGTAC - 10020
- Q D V S P K S F Y R K G S P F Q L P T Y
- K T S H Q N P F T V R A V R F N F P R T
- R R L T K I L L P * G Q S V S T S H V P
10021 - CATGTTTCATTGGACACCTTGATGTTGAGAATTACCTAACCAACCTACTGTGTCATATG - 10080
- H V H W T P * C * E L P N T N L L C H M
- M F I G H L D V E N Y L T P T Y C V I *
- C S L D T L M L R I T * H Q P T V S Y D
10081 - ACAGGTTCTGTACAGTAAACGTGTCGTCTTCTGTACGAATTAGGATTGATACTTCTAGAC - 10140
- T G S V Q * T C R L L Y E L G L I L L D
- Q V L Y S K R V V F C T N * D * Y F * T
- R F C T V N V S S S V R I R I D T S R R
10141 - GAGTAACCGTTTAGGTTGGTATCGAAAGAACAAGTCCGACCGTTACAAGTTGAAGCACAA - 10200
- E * A F R L V S K E Q V R P L Q V E A Q
- S K R L G W Y R K N K S D R Y K L K H N
- V S V * V G I E R T S P T V T S * S T I
10201 - TAACCGGTAAGATACGTTTAAACAGACGAATCCGAATTTCAACTATGAAGATTGGGATTC - 10260
- * P V R Y V L T D E S E F Q L * R L G F
- N R * D T F * Q T N P N F N Y E D W D S
- T G K I R F N R R I R I S T M K I G I L
10261 - TGTGGTTTCATATTTAAACAGGCATAGGTTGGACCAAGTTGTAAAAGTCAAGATCGTACG - 10320
- C G F I F K Q A * V G P V C K S Q D R T
- V G S Y L N R H R L D Q F V K V K I V R
- W V H I * T G I G W T S L * K S R S Y D
10321 - ATGTTACCAAGTGGTAGACCACAAATAGTCACACGCTACTCTGGATTAGTATGGTAATTT - 10380
- M L P S G R P Q I V T R Y S G L V W * F
- C Y Q V V D H K * S H G T L D * Y G N F
- V T K W * T T N S H T V L W I S M V I S
10381 - CCAAGAAAGGAATTACCTAGTACACCACAAACCAAAATTGTAACATACTAACGCAC - 10440
- P R K E L P S T P S Q P K L * L I L T H
- Q E R N Y L V H H H N Q N C N * Y * R T
- K K G I T * Y T I T T K I V T N T N A Q
10441 - AGAAAGACGATATACGTAGTATACCTCGAAGGTTGCTCTCATGTGCGACCATGACTGAAT - 10500
- R K T I Y V V Y L E G C P H V R P * L N
- E R R Y T * Y T S K V V L M C D H D * I
- K D D I R S I P R R L S S C A T M T E S
10501 - CTTCCATTAAAGATACCAGGTAAACAACCTGTCTGTTGACGTGTCCGACGTCCATGTCTG - 10560
- L P F K I P G K Q L S V * R V R R P C L
- F H L R Y Q V N N C L F D V S D V H V C
- S I * D T R * T T V C L T C P T S M S V
10561 - TGTGGTATTGTAATTTACAAAACCGTACCGACATACGACGACAATAGTTACCACTATCC - 10620
- C W Y C N L Q N R T D I R R Q * L P L S
- V G I V I Y K T V P R T Y D D N S Y H Y P
- L V L * F T K P Y R H T T T I V T I H
10621 - ACCAAAGAATTATCTAAGTGGTGATGAACTTACTGAAATTGGAACACCGTTACTTCATG - 10680
- T K E L S K W * * N L L K L E H R Y F M
- P K N Y L S G D E T Y * N W N T V T S C
- Q R I I * V V M K L T E I G T P L L H V
10681 - TTGATACTTGAAACTGTGTTCTAGTACAACCTGTATAACCTGGAGAAAGACGAGTTTGT - 10740
- L I L G N C V L V Q L Y N P G E R R V C
- * Y L E T V F * Y N C I T L E K D E F V
- D T W K L C S S T T V * P W R K T S L S
10741 - CCTTAACGGCAGAATCTATACACACGACGAACTTTCTCGACGACGTCTTACCATACTTA - 10800
- P * R Q N L Y T R R N F L D D V L P Y L
- L N G R I Y T H D E T F S T T S Y H T Y
- L T A E S I H T T K L S R R R L T I L T

FIG. 5 Cont'd

10801 - CCAGCATGATAGGAACCATCGTGATAAAATCTTCTACTCAAATGTGGTAAACTACAACAA - 10860
- P A * * E P S * * N L L L K C G K L Q Q
- Q H D R N H R D K I F Y S N V V N Y N N
- S M I G T I V I K S S T Q M W * T T T I
10861 - TCTGTTACGAGACCACAATGGAAGGTTCCATTCAAGTTCTTTTAAACAATTCCCGTGAGTA - 10920
- S V T R P Q W K V P F K F F * Q F P * V
- L L R D H N G R F H S S S F N N S R E *
- C Y E T T M E G S I Q V L L T I P V S S
10921 - GTAACTACGAAAATTGAAAGAACTGTAGTGATAACTAAGAACAAGTTTCATGTGTCACC - 10980
- V T Y E N * K N C S D N * E Q V S C V T
- * P T K I E R T V V I T K N K F H V S P
- N L R K L K E L * * * L R T S F M C H Q
10981 - AGTGACAAAAGAAACAATGCTCTTACGAAAGAACGGTAAATGAGAACCATAATACCGT - 11040
- S D K K K K Q M L L R K N G K * E P * Y R
- V T K R N K C S Y E R T V N E N H N T V
- * Q K E T N A L T K E R * M R T I I P L
11041 - TAACGACGTACACGATACGACGAACAATTCGTATTCTGTCGTAAGAACACGAACAAGAC - 11100
- * R R T R Y D E Q F V F V R K N T N K D
- N D V H D T T N N S Y S C V R T R T K T
- T T Y T I R R T I R I R A * E H E Q R Q
11101 - AATGGAAGAGAACGTTGTCAACGAATGAAATTATACCAGATGTACGGACGATCGACCCAC - 11160
- N G R E R C Q R M K L Y Q M Y G R S T H
- M E E N V V N E * N Y T R C T D D R P T
- W K R T L S T N E I I P D V R T I D P L
11161 - TACGCATAGTACTGTACCGAACTTAACCGACTGTGATCGAACAGACCAATATCCGAATTC - 11220
- Y A * Y C T E L N R L * S N R P I S E F
- T H S T V P N L T D C D R T D Q Y P N S
- R I V L Y R T * P T V I E Q T N I R I P
11221 - CTAACACAATACATACGAAAGTCGAAATCAAACGAATAAGAGTACTGTGAGCGTGACAA - 11280
- L T Q Y I R S R N Q N E * E Y C R A * Q
- * H N T Y E V E I K T N K S T V E R D K
- N T I H T K S K S K R I R V L S S V T N
11281 - ATACTACTACGACGATCTGCACAAACCTGTGACTACTTACAGTAATGTGAACAAATGTTT - 11340
- I L L R R S A Q T C D Y L Q * C E Q M F
- Y Y Y D D L H K P V T T Y S N V N K C F
- T T T T I C T N L * L L T V M * T N V S
11341 - CAGATGATACCATTACGAAATCTAGTTCGATAAAGGTACACCCGGAATCAATAAAGACAT - 11400
- Q M I P L R N L V R * R Y T R N Q * R H
- R * Y H Y E I * F D K G T P G I N K D I
- D D T I T K S S S I K V H P E S I K T L
11401 - TGGAGATTGATAAGACCACAGCAATGCTGATAGTACAAAAATCGATCTCGATATCACAAA - 11460
- W R L I R P Q Q C * * Y K N R S R Y H K
- G D * * D H S N A D S T K I D L D I T N
- E I D K T T A M L I V Q K S I S I S Q T
11461 - CACACACAACCTCATAATGGGTAAACAATAAATAATGACCGTTGTGGAATGTCACATAGTAC - 11520
- H T Q L I M G N N K * * P L W N V T * Y
- T H N S * W V T I N N D R C G M S H S T
- H T T H N G * Q * I M T V V E C H I V R
11521 - GAACAAATAACAAAGAATCCGATAACAACGACGACGATGAAACCGGAAAAGACAAATGAG - 11580
- E Q I T K N P I T T T T M K P E K T N E
- N K * Q R I R * Q R R R * N R K R Q M S
- T N N K E S D N N D D D E T G K D K * V
11581 - TTGGCAATGAAGTCCGAATGAGAACCACAAATACTGATGAACCAGAGATGTGTTCTTAAA - 11640
- L A M K S E * E P Q I L M N Q R C V L K
- W Q * S P N E N H K Y * * T R D V F L N
- G N E V R M R T T N T D E P E M C S * I
11641 - TCCATATACTTGAGGGTCCCCGAAAACGGAGGATTCTCATCATAACTACGAAAGTTCGAA - 11700
- S I Y L R V P E N G G F S S * L R K F E
- P Y T * G S P K T E D S H H N Y E S S N
- H I L E G P R K R R I L I I T T K V R I

FIG. 5 Cont'd

11701 - TTGTAATTCAACAACCCATAACCTCCATTTGGTACATAGTTCCAACGATGACATGTCAGA - 11760
- L * F N N P * P P F G T * F Q R * H V R
- C N S T T H N L H L V H S S N D D M S D
- V I Q Q P I T S I W Y I V P T M T C Q I
11761 - TTTTACAGACTGCATTTACCGTGTAGACACCATGACGAGAGCCAGAAGTTGTTGAATCT - 11820
- F Y R L H F T C R H H D E S Q E V V E S
- F T D C I S R V D T M T R A K K L L N L
- L Q T A F H V * T P * R E P R S C * I S
11821 - CATCTCAGTAGAAGATTTAACACCCGTGTTACACATGTTGAGGTGTTACTATAAGAAGAA - 11880
- H L S R R F N T R V T H V E V L L * E E
- I S V E D L T P V L H M L R C Y Y K K N
- S Q * K I * H P C Y T C * G V T I R R T
11881 - CGTTTTCTGTGTTGACTTCGAAAGCTCTTCTACCAAAGAGAAAAACAGACAAAACGATAGG - 11940
- R F L C * L R K L F Y Q R E N R Q N D R
- V F C V D F E S S S T K E K T D K T I G
- F S V L T S K A L L P K R K Q T K R * V
11941 - TACGTCCACGACATCTGTAATTATCCAACAGCTCCTTTACGAGCTATTGGCACCATGA - 12000
- Y V P R H L * L S N T L L Y E L L A R *
- T S H D I C N Y P T R S F T S Y W H D E
- R P T T S V I I Q H A P L R A I G T M R
12001 - GAAGTCCGATAACGAAGTCTTAAATCAAGAAATGGTAGTATACGGCGAATACGGTGACGG - 12060
- E V R * R S L K S R N G S I R R I R * R
- K S D N E V L N Q E M V V Y G E Y G D G
- S P I T K S * I K K W * Y T A N T V T G
12061 - GTCCTCCGGATACTCGTCCGACATCGATTACCACTAAGACTTCAGCAAGAGTTTTTCAAT - 12120
- V L R I L V R H R L P L R L Q Q E F F N
- S S G Y S S D I D Y H * D F S K S F S I
- P P D T R P T S I T T K T S A R V F Q F
12121 - TTCTTTAGAACTTACACCGATTAGACTCAAAGTGGCACTACGACGGTACGTTGCGTTC - 12180
- F F R N L H R F R L K L A L R R Y V A F
- S L E T Y T D L D S N W H Y D G T L R S
- L * K L T P I * T Q T G T T T V R C V Q
12181 - AACCTTTTCTACCGTCTAGTCCGATACTGGGTTTACATGTTTGTCCGTCTAGACTCCTG - 12240
- N L F Y R L V R Y W V Y M F V R S R L L
- T F S T V * S D T G F T C L S V L D S C
- P F L P S S P I L G L H V C P F * T P V
12241 - TTCTCCCGTTTTTCATTGATCACGATACGTTTGTGTACGAGAAGTGATACGAATCCTTCGAA - 12300
- F S R F H * S R Y V C Y E K * Y E S F E
- S P V F I D H D T F V T R S D T N P S N
- L P F S L I T I R L L R E V I R I L R T
12301 - CTATTACTACGTGAATTGTTGTAATAGTTGTGTACGCGCACTACCAACACAAGGTGAGTTG - 12360
- L L L R E L L * * L L R A L P T Q G E L
- Y Y Y V N C C N S C Y A H Y Q H K V S C
- I T T * I V V I V V T R T T N T R * V V
12361 - TAGTATGGTAACTGATGTCGTCGGTTTTGAGTACCAACAACAGGGACTAATACCATGGATG - 12420
- * Y G N * C R R F E Y Q Q Q G L I P W M
- S M V T D V V G L S T N N R D * Y H G C
- V W * L M S S V * V P T T G T N T M D V
12421 - TTCTTGTGAACACTACCATTGTGGAATGTATACGTAGACGTGAGACCCTTTAGGTGCGTT - 12480
- F L * T L P L W K C I R R R E T L * V V
- S C E H Y H C G N V Y V D V R P F R S F
- L V N T T I V E M Y T * T * D P L G R S
12481 - CAACAACACTACGCCTATCGTTCTAACAAGTTGAATCACTTTAATTGTACCTGTTAAGTGGT - 12540
- Q Q L R L S F * Q V E S L * L Y L L S G
- N N Y A Y R S N K L N H F N C T C * V V
- T T T P I V L T S * I T L I V P V K W F
12541 - TTAAACCGAACCGGAGAATAACAATGTGCGAGATTCTCGGTTGAGTCGACAATTGATGTC - 12600
- L N R T G E * Q C R D S R L S R Q F D V
- * T E P E N N N V E I L G * V D N L M S
- K P N R R I T M S R F S V E S T I * C L

FIG. 5 Cont'd

12601 - TTATTACTTGACTCAGGTCATCGTGATGCTGTCTACAGGACACGCCGACCATGGTGTGTT - 12660
- L L L D S G H R D A V Y R T R R P W C V
- Y Y L T Q V I V M L S T G H A D H G V F
- I T * L R S S * C C L Q D T P T M V C L
12661 - TGTCGAACATGACTACTGTTACGTGAACGGATGATATTGTTAAGCTTCCCTCCATCCAAA - 12720
- C R T * L L L R E R M I L L S F P P S K
- V E H D Y C Y V N G * Y C * A S L H P N
- S N M T T V T * T D D I V K L P S I Q T
12721 - CACGACCGTAATGATAGTCTGGTGGTTCTAGAGTTTACCCGATCTAAGGGATTCTCACTA - 12780
- H D R N D S L V V L E F T R S K G F S L
- T T V M I V W W F * S L P D L R D S H Y
- R P * * * S G G S R V Y P I * G I L T T
12781 - CCATGTCCATGTTAAATGTGTCTTGACCTTGGTGGAACATCCAAACAATGTCTGTGGT - 12840
- P C P C * M C L D L G G T S K Q C L C G
- H V H V K C V L T L V E H P N N V C V V
- M S M L N V S * P W W N I Q T M S V W F
12841 - TTCCCCGATTTCACCTTATGAACATGAAGTAGTTTCCGAATTTGTTGGATTATCTCCA - 12900
- F P G F H F M N M K * F P N L L D L S P
- F P D F T L * T * S S F R I C W I Y L H
- S R I S L Y E H E V V S E F V G F I S I
12901 - TACCACGACCCGTCAAATCGACGATGTCATGCAGAAAGTCCGACCTTTACGATGTCTTCAT - 12960
- Y H D P S N R R C H A E V R P L R C L H
- T T T R Q I D D V M Q K S D L Y D V F M
- P R P V K S T M S C R S P T F T M S S W
12961 - GGACGGTTAAGTTGACACGAAAGGAAGACACGAAACGTCATCTGGGACGATTTCGTATA - 13020
- G R L S * H E R K T R K R H L G R F R I
- D G * V D T K G R H E N V I W D D F V Y
- T V K L T R K E D T K T S S G T I S Y I
13021 - TTCCTAATGGATCGTTCACCTCCTGTTGGTTAGTGGTTGACACACTTCTACAACACATGT - 13080
- F L M D R S P P V G * W L T H F Y N T C
- S * W I V H L L L V S G * H T S T T H V
- P N G S F T S C W L V V D T L L Q H M C
13081 - GTGTGACCATGTCTGTCCGTTAATGACATTGTGGTCTTCGATTGTACCTGGTTCTCAGG - 13140
- V * P C P V R * * H C G L R L Y L V L R
- C D H V L S V N D I V V F D C T W F S G
- V T M S C P L M T L W S S I V P G S Q E
13141 - AAACCACCACGAAGTACAACAGACATAACATCTACGGTGTAAGTGGTAGGTTTAGGATTT - 13200
- K P P R S T T D I T S T V * L V G L G F
- N H H E V Q Q T * H L R C N W * V * D F
- T T T K Y N R H N I Y G V T G R F R I S
13201 - CCTAAGACACTGAACTTTCCATTCATGCAGGTTTATGGATGGTGAACACGATTACTGGGT - 13260
- P K T L N F P F M Q V Y G W * T R L L G
- L R H * T F H S C R F M D G E H D Y W V
- * D T E L S I H A G L W M V N T I T G S
13261 - CACCCAAAATGTGAATCTTTGTGTCAGACATGGCAGACGCCTTACACCTTTCCAATACCG - 13320
- H P K C E S L C Q T W Q T P Y T F P I P
- T Q N V N L C V R H G R R L T P F Q Y R
- P K M * I F V S D M A D A L H L S N T D
13321 - ACATCAACACTGGTTGAGGCGCTTGGGAACTACGTCAGACGCCTACGTAGTTGCAAAAAT - 13380
- T S T L V E A L G N Y V R R L R S C K N
- H Q H W L R R L G T T S D A Y V V A K I
- I N T G * G A W E L R Q T P T * L Q K F
13381 - TTGCCCCAACGCCACATTACGTCGGGCGAATGTGGCAGCGGTGTCGGTGATCATGAC - 13440
- L P K R H I H V G Q N V A R R V R D H D
- C P N A T F T S G R M W H A V S V I M T
- A Q T P H S R R A E C G T P C P * S * L
13441 - TACAGCAGATGTCCCGAAAACATATAAATGTTGCTTTTCAACGACCAAAACGTTTCAAGG - 13500
- Y S R C P E N Y K C C F F N D Q N V S R
- T A D V P K T I N V A F S T T K T F Q G
- Q Q M S R K L * M L L F Q R P K R F K D

FIG. 5 Cont'd

13501 - ATTTTGGATTAACGACAGCGAAGGCTCTTCTCTACTCTCCGTTAAATAATCTGAGAA - 13560
- I F D * R Q R R S S S Y S F R * I I * E
- F L I N D S E G P L P T P S V K * S E N
- F * L T T A K V L F L L P L N N L R M
13561 - TGAAACATCAATTCTCCGTATGATACAGATTGATGGTTGTACTTCTCTGATAAATATTGA - 13620
- * N I N S P Y D T D * W L Y F S D K Y *
- E T S I L R M I Q I D G C T S L I N I E
- K H Q F S V * Y R L M V V L L * * I L N
13621 - ACCAATTTCTAACAGGTCGCCAACGACAGGTACTGAAAAAGTTCAAATCTCATCTACCAC - 13680
- T N F * Q V A N D R Y * K S S N L I Y H
- P I S N R S P T T G T E K V Q I S S T T
- Q F L T G R Q R Q V L K K F K S H L P L
13681 - TGTACCATGGTGTATATAGTGCAGTCGAGATTGATTATGTGTACCGACTAAATCAGA - 13740
- C T M V Y I V Q S Q I D L C V T D * I R
- V P W C I * C S R R L I Y V L P T K S D
- Y H G V Y S A V A D * F M C Y R L N Q I
13741 - TACGAGATGCAGTAAACTACTCCATTAACTATGTAATTTCTTTATGAGCAGTGTA - 13800
- Y E M Q * N Y S H * H Y V I F F M S S V
- T R C S K T T P I N T M * F S L * A V Y
- R D A V K L L P L T L C N F L Y E Q C M
13801 - TGTTAACGACACTACTACTAATAAAGTTATCTTCTTAACCATGAAAGCATCTCTTAG - 13860
- C * R H Y Y * * S Y S S * P Y * S I S *
- V N D T T T N K V I L P N H T E A S L R
- L T T L L L I K L F F L T I L K H L L G
13861 - GACTGTAGAATGCGCATATACGATTGAATCCACTCGCACATGCGGTTAGTAATAATTTCT - 13920
- D C R M R I Y D * I H S H M R L V I I S
- T V E C A Y T I E S T R T C G * * * F L
- L * N A H I R L N P L A H A V S N N F *
13921 - GACATGTTAAGACGCTACGATACGCACTACGTCCGTAACATCCGCATGACTGTAATCTAT - 13980
- D M L R R Y D T H Y V R N I R M T V I Y
- T C * D A T I R T T S V T S A * L * S I
- H V K T L R Y A L R P * H P H D C N L L
13981 - TAGTCCTAGAATTACCTTGACCATGCTAAAGCCACTAAAGCATGTTTCATCGTGGTCCGA - 14040
- * S * N Y P * P C * S H * S M F I V V R
- S P R I T L D H A K A T K A C S S W S D
- V L E L P L T M L K P L K H V H R G P T
14041 - CGCCTCAAGGATAACACCTAAGTATAATGAGTAACGACTACGGGTAGGAGTGAACTGAT - 14100
- R L K D N T * V * * V T T T G R S E T D
- A S R I T P K Y N E * R L R V G V K L I
- P Q G * H L S I M S N D Y G * E * N * S
14101 - CCCGTAACCGACGACTCAGGGTATACCTACGACTAGAGCGTTTGGTGAATAATTCACCC - 14160
- P V T D D S G Y T Y D * S V L V N N S P
- P * P T T Q G I P T T R A F W * I I H P
- R N R R L R V Y L R L E R F G E * F T L
14161 - TAAACGACTTTATACTAAAATGCCTTCTCTGAAACAGAGAAGCTGGCAATAAAATTTA - 14220
- * T T L Y * N A F S L K Q R S W Q * N L
- K R L Y T K M P S L * N R E A G N K I Y
- N D F I L K C L L S E T E K L A I K F I
14221 - TAACCCTGGTCTGTATGGTAGGGTTAACATAATTGACAAACCTACTATCCACATAGGAAG - 14280
- * P W S V W * G * H N * Q T Y Y P H R K
- N P G L Y G R V N I I D K P T I H I G S
- T L V C M V G L T * L T N L L S T * E V
14281 - TAACACGTTTGAATTAACACAATAAAAGATGACACAAAGGTGGATGTTCAAAACCTGGTG - 14340
- * H V * N Y T I K D D T K V D V Q N L V
- N T F E I T Q * K M T Q R W M F K T W *
- T R L K L H N K R * H K G G C S K P G D
14341 - ATCATTCTTTTATAAACATCTACCACAAGGAAACAACAAAGTTGACCTATGGTAAAAG - 14400
- I I L F I N I Y H K E N N K V D L W * K
- S F F L * T S T R K T T K L T Y G K S
- H S F Y K H L P Q G K Q Q S * P M V K A

FIG. 5 Cont'd

14401 - CACTCAATCCTCAGCATGTATTAGTCCTACATTTGAATGTATCGAGCGCAGAGTCAAAGT - 14460
- H S I L S M Y * S Y I * M Y R A Q S Q S
- T Q S S A C I S P T F E C I E R R V K V
- L N P Q H V L V L H L N V S S A E S K F
14461 - TCCTTGAAAATCACATACGACGACTAGGTCGATACGTACGTCGAAGACCGTTAAATAACG - 14520
- S L K I T Y D D * V D T Y V E D R * I T
- P * K S H T T T R S I R T S K T V K * R
- L E N H I R R L G R Y V R R R P L N N D
14521 - ATCTATTGCGTGATGTACGAAAAGTCATCGACGTGATTGTTTGTACAACGAAAAGTTT - 14580
- I Y L R D V R K V I D V I V C Y N E K F
- S I C V M Y E K S S T * L F V T T K S L
- L F A * C T K S H R R D C L L Q R K V *
14581 - GACAGTTGGGCCATTAAAATTATTTCTGAAAATACTGAAACGACACAGATTCCAAAGA - 14640
- D S L G H * N Y F * K Y * N D T D F Q R
- T V W A I K I I S E N T E T T Q I S K E
- Q F G P L K L F L K I L K R H R F P K K
14641 - AATTCCTTCCTCAAGACAACCTTGATTTGTGAAGAAGAAACGAGTCCTACCGTTGCGAC - 14700
- N S F L Q D N L I L * R R N E S Y R C D
- I P S F K T T * F C E E E T S P T V A T
- F L P S R Q L D F V K K K R V L P L R R
14701 - GATAGTCACTAATACTGATAATAGCAATATTAGACGGTTGTTACACACTATAGTCTGTG - 14760
- D S H * Y * * * Q Y * T V V T H Y S L L
- I V T N T D N S N I R R L L H T I V C *
- * S L I L I I A I L D G C Y T L * S V E
14761 - AGGATAAGCATCAACTTCAACAACCTATTATGAACTAACAATGCTACCACCGACATAAT - 14820
- R I S I N F N N Y L * N * Q C Y H R H N
- G * A S T S T T I Y E T N N A T T D I I
- D K H Q L Q Q L F M K L T M L P P T * L
14821 - TACGGTTGGTTCAATTAGCAATTGTTAGACCTATTTAGTCGACCAAAGGGTAAATTATTTA - 14880
- Y G W F I S N C * T Y L V D Q R V N Y L
- T V G S L A I V R P I * S T K G * I I Y
- R L V H * Q L L D L F S R P K G K L F T
14881 - CCCCATTCGATCTGAAATAATACTGAGTTACTCAATACTCCTAGTTCTACGTGAAAAGC - 14940
- P H S D L K * Y * V T Q Y S * F Y V K S
- P I P I * N N T E L L N T P S S T * K A
- P F R S E I I L S Y S I L L V L R E K R
14941 - GCATATGATTTCGATTACAGTAGGGATGATATTGAGTTTACTTAGAATTCATACGGTAAT - 15000
- A Y D S H Y S R D D I E F T * N S Y G N
- H M I R I T V G M I L S L L R I H T V I
- I * F A L Q * G * Y * V Y L E F I R * S
15001 - CACGTTTCTTATCTCGAGCGTGGCATCGACCAGAGATAGACATCATGATACTGTTTAT - 15060
- H V S Y L E R G I D H R D R H H D T V Y
- T F L I S S V A S T T E I D I M I L F I
- R F L S R A W H R P Q R * T S * Y C L S
15061 - CTGTCAAAGTAGTCTTTAATAACTTCAGTTATCGGCGGTGATCTCCTCGATGACACCATT - 15120
- L S K * S L I T S V I G G D L L D D T I
- C Q S S L * * L Q L S A V I S S M T P L
- V K V V F N N F S Y R R * S P R * H H *
15121 - AACCTTGTTTCGTTCAAAATGCCACCGACCGTATTATACAATTTTGTACAAATGTCACTAC - 15180
- N L V R S K C H R P Y Y T I F D K C H Y
- T L F V Q N A T D R I I Q F L T N V T T
- P C S F K M P P T V L Y N F * Q M S L H
15181 - ATCTTTGAGGTGTGGAATACCCAACCCTAATAGGTTTTACACTGTCTCGGTACGGATTGT - 15240
- I F E V W N T Q P * * V L H C L G T D C
- S L R C G I P N P N R F Y T V S V R I V
- L * G V E Y P T L I G F T L S R Y G L Y
15241 - ACGAATCCTATTACCGGAGAGAACAAGAACGAGCGTTTGTATTGTGAACGACATTGAATA - 15300
- T N P I T G E N K N E R L Y C E R H * I
- R I L L P E R T R T S V C I V N D I E *
- E S Y Y R R E Q E R A F V L * T T L N S

FIG. 5 Cont'd

15301 - GTGTGGCAAAGATGTCCAATCGATTGCTCACACGCGTTTCATAATTCCTACTCTACCACTACA - 15360
- V W Q R C P I D C S H A F I I H S T S T
- C G K D V Q S I A H T R S * F T L P V H
- V A K M S N R L L T R V H N S L Y Q Y T
15361 - CACCGCCGAGTGATATACAATTTGGTCCACCTTGTAGTAGGCCACTACGATGTTGACGAA - 15420
- H R R V I Y N L V H L V V G H Y D V D E
- T A E * Y T I W S T L * * A T T M L T N
- P P S D I Q F G P P C S R P L R C * R I
15421 - TACGATTATCAGAAATGTAAACAGTTTCGCAATGTTCGGTTACATTTACGTGAAGAAA - 15480
- Y D Y H R N C K Q F D N V G Y I Y V K K
- T I I T E I V N S S T M S V T F T * R K
- R L S Q K L * T V R Q C R L H L R E E S
15481 - GTTGACTACCATTATTCTATCGACTGTTTCATACAGGCGTTAGATGTTGTGTCCGAGATAC - 15540
- V D Y H Y S I D C S Y R R * M L C P R Y
- L T T I I L S T V H T G V R C C V R D T
- * L P L F Y R L F I Q A L D V V S E I L
15541 - TCACAGAGATATCTTTATCCCTACAAGTACTTAAGCACCTACTCAAAATGCGAATGG - 15600
- S Q R Y L Y P Y N * Y L S T Y S K C E W
- H R D I F I P T T S T * A P T Q N A N G
- T E I S L S L Q L V L K H L L K M R M D
15601 - ACGCATTGTGTAAGAGGTACTACTAAGAAAGACTACTACGGCAACACACGATATTGTCAT - 15660
- T H L * R G T T K K D Y Y G N T R Y C H
- R I C K E V L L R K T T T A T H D I V I
- A F V K R Y Y * E R L L R Q H T I L S L
15661 - TGATACGCCGAGTTCCAAATCATCGATCGTAATTCTTGAAATTCGGTCAAGAAATAATAG - 15720
- * Y A E F Q I I D R N S * N S V K K * *
- D T P S S K S S I V I L E I P S R N N S
- I R R V P N H R S * F L K F R Q E I I V
15721 - TTTTATTACACAAGTACAGACTCCGTTTACAACCTGACTCTGACTGGAATGATTTCTCG - 15780
- F Y Y T S T D S V L Q P D S D W N D F L
- F I T Q V Q T P F Y N L T L T G M I S W
- L L H K Y R L R F T T * L * L E * F P G
15781 - GAGTGTCTAAACGAGTGTGCTATGTTACGATCAATTTGTTCTCTACTAATGCACATGG - 15840
- E C L K R V S Y V T I N L F L Y * C T W
- S A * N E C R M L R S I C S S T N A H G
- V L K T S V V C Y D Q F V P L L M H M D
15841 - ACGGAATGGGTCTAGGTAGTTCTTATAATCCGCGTCCGACAAAACAGCTACTATAACAGT - 15900
- T E W V * V V L I I R V R Q N S Y Y N S
- R N G S R * F L * S A S D K T A T I T V
- G M G L G S S Y N P R P T K Q L L * Q F
15901 - TTTGTCTACCATGTGAATACTAATTTCCAAGCACAGTGACCGATAACTACGAATGGGTG - 15960
- F V Y H V N T N F P S T V T D N Y E W V
- L S T M * I L T F Q A Q * P I T T N G *
- C L P C E Y * L S K H S D R * L R M G E
15961 - AATGTTTTGTAGGATTAGTCCTCATACGACTACAGAAAGTGAACATAAATGTTATGTAAT - 16020
- N V L * D * S S Y D Y R K * T * M L C N
- M F C R I S P H T T T E S E H K C Y V I
- C F V G L V L I R L Q K V N I N V M * S
16021 - CTTTCAATGTACTACTCGAATGACCGGTGTACAACCTGTACATAAGGCATTACGATTGAT - 16080
- L S M Y Y S N D R C T T C T * G I T I D
- F Q C T T R M T G V Q P V H K A L R L I
- F N V L L E * P V Y N L Y I R H Y D * L
16081 - TACTATTGTGGAGTGCCATGACCCTTGGACTCAAAATACTCCGATACATGTGTGGTGTAT - 16140
- Y Y C G V P * P L D S K Y S D T C V V Y
- T I V E C H D P W T Q N T P I H V W C M
- L L W S A M T L G L K I L R Y M C G V C
16141 - GTCAGAACGTCCGACATCCACGAACACATAACACGTTAAGTGTCTGAAGTGAAGCAACGC - 16200
- V R T S D I H E H I T R * V S E V K Q R
- S E R P T S T N T * H V K C L K * S N A
- Q N V R H P R T H N T L S V * S E A T P

FIG. 5 Cont'd

16201 - CACGGACATAATCCTCTGGTAAGGATACAACGTTACGACGATACTGGTACAGTAAAGTT - 16260
- H G H N P L V R I Q R S R R Y W Y S K V
- T D I I L W * G Y N V H D D T G T V K L
- R T * S S G K D T T F T T I L V Q * S C
16261 - GTAGTGTGTTTAATCACAACAGACAATTAGGGATACAAACGTTACGGGGTCCAACACTAC - 16320
- V V C L I T T D N * G Y K R Y G V Q H Y
- * C V * S Q Q T I R D T N V T G S N T T
- S V F N H N R Q L G I Q T L R G P T L Q
16321 - AGTGACTACACTGTGTTGACATAGATCCTCCATACTCGATAATAACGTTACAGTGATTTCG - 16380
- S D Y T V L T * I L H T R * * R S V Y S
- V T T L C * H R S S I L D N N V Q C I R
- * L H C V D I D P P Y S I I T F S V F G
16381 - GAGGGTAATCAAAGGTAATACACGATTACCAGTCCAAAACCAAATATGTTTTGTGTA - 16440
- E G N Q K V I H D Y Q S K N Q I C F C V
- R V I K R * Y T I T S P K T K Y V F V Y
- G * S K G N T R L P V Q K P N M F L C T
16441 - CACATCCGTCACTGTTACAGTGACTGAAGTTACGCTATCGTTGTACACTAACCTGATTAC - 16500
- H I R H C Y S D * S Y A I V V H * P D Y
- T S V T V T V T E V T L S L Y T N L I T
- H P S L L Q * L K L R Y R C T L T * L R
16501 - GACCCTAATGTATGAACGGTTGTGAACATGACTCTCTGAGTTCGAAAAGCGTCGTCTTT - 16560
- D R * C M N G C E H D S L S S K S V V F
- T A N V * T V V N M T L * V R K A S S L
- P L M Y E R L * T * L S E F E K R R L C
16561 - GCGAGTTTCGGTGACTCCTTTGTAAATTCGACAGTATACCATAACGGTGACATGCGCTTC - 16620
- A S F G D S F V N S T V Y H N G D M R F
- R V S V T P L * I R Q Y T I T V T C A S
- E F R * L L C K F D S I P * R * H A L H
16621 - ATGAGAGACTGTCTCTTAACGTAGAAAGTACCCTCCAACCTTTTGGATCTGGTGGTAACT - 16680
- M R D C L L T * K V P S N L L D L V V T
- * E T V S * R R K Y P P T F W I W W * L
- E R L S L N V E S T L Q P F G S G G N L
16681 - TGTCTTTGATACAGAAATGACCAATGGCACATTGATTTTTATCATTTTCATGTCTAACCTC - 16740
- C L * Y R N D Q W H I D F Y H F M S N L
- V F D T E M T N G T L I F I I S C L T S
- S L I Q K * P M A H * F L S F H V * P L
16741 - TCATGTGGAACTTTTTCCACTGATACCACTACGACAACACATGTCTCCATGATGCTGTA - 16800
- S C G N F F H * Y H Y D N T C L H D A V
- H V E T F S T D T T T T T H V S M M L Y
- M W K L F P L I P L R Q H M S P * C C M
16801 - TGTTCAACTTACAACCACTAATGAAACACAACGTAGAGTGTGACATTACGGTGAATCAC - 16860
- C S T Y N H * * N T T V E C D I T V N H
- V Q L T T T N E T Q L * S V T L R * I T
- F N L Q P L M K H N C R V * H Y G E S R
16861 - GTGGATGAGATCACGGTGTCTCGTGATACACTCTTAATGACCGAACATGGGTTGTGAGT - 16920
- V D E I T V F S * Y T L N D R T W V V S
- W M R S R C S R D T L L M T E H G L * V
- G * D H G V L V I H S * * P N M G C E L
16921 - TGTAGAGTCTACTCAAAGATCGTTACAACGTTAATAGTTTTCCAGCCGTACGTTTTCA - 16980
- C R V Y S K D R Y N V * * F S S R T F S
- V E S T Q K I V T T F N S F P A V R F H
- * S L L K R S L Q R L I V F Q P Y V F M
16981 - TGAGATGTGAGGTTCCCTGGTGGACCATGACCATCTCAGTAAAACGGTAGCCTGAACGAG - 17040
- * D V R F L V D H D H S Q * N G S L N E
- E M * G S W W T M T I L S K T V A * T R
- R C E V P G P * P F S V K R * P E R E
17041 - AGATAATGGGTAGACGAGCGTATCACATATGCCGTACGAGAGTACGTCGACAACTACGGG - 17100
- R * W V D E R I T Y A V R E Y V D N Y G
- D N G * T S V S H M P Y E S T S T T T G
- I M G R R A Y H I C R T R V R R Q L R D

FIG. 5 Cont'd

17101 - ATACACTTTTCCGTAATTTTATAAACGGGTATCTATTACATCATCTTAGTATGGACGCG - 17160
- I H F S V I L * T G I Y L H H L S M D A
- Y T F P * F Y K R V S I Y I I L V W T R
- T L F R N F I N G Y L F T S S * Y G R A
17161 - CACGCGCGCATCTCACAAACTATTTAAGTTTCACTTAAGTTGTGATCTTGTACATACAAA - 17220
- H A R I S Q N Y L S F T * V V I L S Y K
- T R A S H K T I * V S L K L * S C H T K
- R A H L T K L F K F H L S C D L V I Q K
17221 - AGACGTGACATTTACGTAACGGTCTTTGTGACGACTGTAACATCAGAACTACTTTAGA - 17280
- R R D I Y V T V F V D D C N I R N Y F R
- D V T F T * R S L L T T V T S E T T L E
- T * H L R N G L C * R L * H Q K L L * R
17281 - GATACCGATGATTAATACTGAACACAGTTACGATCTGAAGCACGTTTGTGATGC - 17340
- D T D D * Y * T H N S Y D L K H V L * C
- I P M I N T E L T T V T I * S T F C D A
- Y R * L I L N S Q Q L R S E A R F V M Q
17341 - AGATATAACCGCTAGGACGAGTTAATGGTCGGGGGGCGTGTAAACGACTGATTTCCGTTGTG - 17400
- R Y N R * D E L M V G G R V T T D F R V
- D I T A R T S * W S G G V * R L I S V *
- I * P L G R V N G R G A C N D * F P C D
17401 - ATCTTGGTCTTATAAAATTAAGTCACACGCTCTGAATACTTTTGTATCCAGGTCTGTACA - 17460
- I L V L * N * V T R L N T F V I Q V C T
- S W S Y K I K S H V * I L L L S R S V Q
- L G L I K L S H T S E Y F C Y P G L Y K
17461 - AGGAACCTTGAACAGCGGCAACAGGACGACTTTAACAACGTGTGACACTCACGAAATCAAA - 17520
- R N L E Q R Q Q D D F N N C D T H E I K
- G T L N S G N R T T L T T V T L T K S N
- E P * T A A T G R L * Q L * H S R N Q I
17521 - TACTGTTATTCGATTTTCGTGTGTTCTCTTCAGTCGAGTTACGAAAGTTTACAAGATGT - 17580
- Y C Y S I F V C S S S V E L R S F T R C
- T V I R F S C V P L Q S S Y E V L Q D V
- L L F D F R V F L F S R V T K F Y K M F
17581 - TTCCACAATAATGTGTACTACAAAGTAGACGTTAGTTGTCTGGAGTTTATCCGCAACATT - 17640
- F H N N V Y Y K V D V S C L E F I R N I
- S T I M C T T K * T L V V W S L S A T F
- P Q * C V L Q S R R * L S G V Y P Q H S
17641 - CTCTTAAAGAATGTGCGTTAGGACGAACCTCTTTTCGACAAAAATAGAGTGAATATTAA - 17700
- L L K N V R * D E P L F D K N R V E Y *
- S * R M C V R T N L F S T K I E W N I K
- L K E C A L G R T S F R Q K * S G I L S
17701 - GTGTCTTGCACATCGAAGTTTGTAGAATCCTAACGGATGCGTCTGACAACTAAGTAGTG - 17760
- V S C D I E V F R I L T D A S D N * V V
- C L A T S K F L E S * R M R L T T K * C
- V L R H R S F * N P N G C V * Q L S S V
17761 - TCCCAAGACTTATACTGATACAGTATAAGTGTGTTTGATGACTTTGTGCGTGTGAGAACAT - 17820
- S Q D L Y * Y S I S V F D D F V V * E H
- P K T Y T D T V * V C L M T L S C E N I
- P R L I L I Q Y K C V * * L C R V R T L
17821 - TACAGTTGGCAAAGTTACACCGATAGTGTCCCGTTTAAACCGTAAACACGTATTACA - 17880
- Y S W Q S Y T D S V P V F N R K T R I T
- T V G K V T P I V F P F L T V K H V L Q
- Q L A K L H R * C S R F * P * N T Y Y R
17881 - GACTATCTCTAGAAATACTGTTTGACGTTAAATGTTTCAGATCTTATGGTGCAGCGTTAC - 17940
- D Y L * K Y C L T L N V Q I F M V Q R Y
- T I S R N T V * R * M F R S L W C S V T
- L S L E I L F L D V K C S D L Y G A A L H
17941 - ACCGATGTAATGTTCTCTTTTACATTGACCTGAAAAATTCCTGACATCATCTAGTAAT - 18000
- T D V M F V F Y I D L K N S * H H S S N
- P M * C S S F T L T * K I P D I I L V M
- R C N V R L L H * P E K F L T S F * * *

FIG. 5 Cont'd

18001 - GACCAGAAGTAGGATGTGTCCGTGGATGTGTGGAGTCGCAACTATATTTCAAGTTCTGAC - 18060
- D Q K * D V S V D V W S R N Y I S S S D
- T R S R M C P W M C G V A T I F Q V L T
- P E V G C V R G C V E S Q L Y F K F * L
18061 - TTCCTAATACACAAGTGTATGGTCCGTATGGTTTCTGTACTGGATGGCATCTGAGTAGA - 18120
- F L I H N C M V R M V S C T G W H L S R
- S * Y T T V W S V W F P V L D G I * V E
- P N T Q L Y G P Y G F L Y W M A S E * R
18121 - GATACTACCCAAAGTTTTACTTAATGGTTCAGTTACCAATGGGATTATACAAATAGTGGG - 18180
- D T T Q S F T * W F S Y Q W D Y T N S G
- I L P K V L L N G S V T N G I I Q I V G
- Y Y P K F Y L M V Q L P M G L Y K * W A
18181 - CGCTTCTTCGATAAGCAGTGCAAGCAGCACCTAACCGAACTACATCTCCCGACAGTAC - 18240
- R F F D K Q C K H A P N R N Y I S R Q Y
- A S S I S S A S T H L T E T T S P D S T
- L L R * A V Q A R T * P K L H L P T V R
18241 - GTTGATCTCTACGACCCCATGATTGGATGGAGAGGTCGATCCTAAAAGATGTCCACAAT - 18300
- V D L Y D T H D W M E R S I L K D V H N
- L I S T T P M I G W R G R S * K M S T I
- * S L R H P * L D G E V D P K R C P Q L
18301 - TGAATCATCGACATGGCTGACCAATACAAGTGTGACTTTTATGTGTCTTAAGTGGTCTC - 18360
- * I I D M A D Q Y N C D F Y C V L S G L
- E S S T W L T N T T V T F I V S * V V S
- N H R H G * P I Q L * L L L C L K W S Q
18361 - AATTACGTTTTGGAGGTGGTCCACTGGTCAAATTTGTAGAATATGGTGAGTACATATTTTC - 18420
- N Y V L E V V H W S N L * N M V S T Y F
- I T F W R W S T G Q I C R I W * V H I S
- L R F G G G P L V K F V E Y G E Y I F P
18421 - CGAACGGGACCTTACATCACGCATAATTCTATCATGTTTACGAGTCACTATGTGACTTTC - 18480
- R T G P Y I T H N S I M F T S H Y V T F
- E R D L T S R I I L S C L R V T M * L S
- N G T L H H A * F Y H V Y E S L C D F P
18481 - CTAACAGTCTGTCTCAGCACAAGCAGGAAACCGCGTACCGAACTCGAATGTAGTTACT - 18540
- L T V C L S T S R K P A Y R N S N V V T
- * Q S V S A Q A G N P R T E T R M * L L
- N S L S Q H K Q E T R V P K L E C S Y F
18541 - TCATGAAACAGTTTCTAACCTGGACTTTCTTGACAACAGACACACTGTTTGACGTTGAA - 18600
- S * N S S N L D F L A Q Q T H C L H V E
- H E T V L T W T F L H N R H T V C T L N
- M K Q F * P G L S C T T D T L F A R * T
18601 - CGAAAAGATGAAGTAGTCTATGAATACGGACGACCTTAGTAAGACACCCAAAAGTATAC - 18660
- R K D E V V Y E Y G R P * * D T Q N * Y
- E K M K * S M N T D D L S K T P K T D T
- K R * S S L * I R T T L V R H P K L I Q
18661 - AGATATTGGGTAAATACTAATACTACAAGTCGTCACCCCGAAATGCCCATGGAAGTCTCAT - 18720
- R Y W V N T N Y K S S P R N A H W K S H
- D I G * I L T T S R H P E M P I G S L I
- I L G K Y * L Q V V T P K C P L E V S L
18721 - TGGTACTGGTTGTAACGGTCCATGTACCTTTACGTGTACACCGATCAACACTACGATAGT - 18780
- W Y W L * R S M Y L Y V Y T D Q H Y D S
- G T G C N G P C T F T C T P I N T T I V
- V L V V T V H V P L R V H R S T L R * Y
18781 - ACTGATCTACAAATCGTCAGGTACTCACGAAACAATTCGCGCAACTAACAGACAACCTTA - 18840
- T D L Q I V R Y S R N N S R N * P D N L
- L I Y K S G T H E T I R A T N Q T Y
- * S T N R Q V L T K Q F A Q L T R Q L M
18841 - TGGGATAATATCCTCTACTTGACTCCCAATTAAGACGAACGTCTTTTCATGTTGTGTACC - 18900
- W D N I L Y L T P N * D E R L F M L C T
- G I I S S T * L P I K T N V F S C C V P
- G * Y P L L D S Q L R R T S F H V V Y Q

FIG. 5 Cont'd

18901 - AACACTTCAGACGTAACGAACGACTATTCAAAGGTCAAGAAGTACTGTAACCTTTAGGTT - 18960
- N T S D V T N D Y S K V K K Y C N L * V
- T L Q T * R T T I Q R S R S T V T F R F
- H F R R N E R L F K G Q E V L * P L G F
18961 - TCCGATAGTTCACACACGGAGTCCGACTTCATCTTACCTTCAAGATGCTACGAGTCGGTA - 19020
- S D S S H T E S D F I L P S R C Y E S V
- P I V H T R S P T S S Y L Q D A T S R Y
- R * F T H G V R L H L T F K M L R V G T
19021 - CATCACTGTTTCGAATGTTTATCTCCTCGAGAAGATAAGAATACGATGTGTAGTGCTAT - 19080
- H H C F E C F I S S R R * E Y D V * C Y
- I T V S N V L S P R E D K N T M C S A I
- S L F R M F Y L L E K I R I R C V V L F
19081 - TTAAGTGACTACCACAAACAAACAAACCTTAACATTGCAACTAGCAATGGGTCGGTTAC - 19140
- L S D Y H K Q T K P * H C N * Q W V G Y
- * V T T T N K Q N L N I A T S N G S V T
- K * L P Q T N K T L T L Q L A M G R L R
19141 - GTTAACACACATCCAAACTGTGTTCTCAGAACAGTTTGAACCTGAATGGTCCGACACTAC - 19200
- V N T H P N C V L R T V * T * M V R H Y
- L T H I Q T V F S E Q F E L E W S D T T
- * H T S K L C S Q N S L N L N G P T L P
19201 - CACCATCAAACATACACTTATTCGTACGTAAGGTGTGAGGTGCGAAAGCTATTTTCACGTA - 19260
- H H Q T Y T Y S Y V R C E V E S Y F H V
- T I K H T L I R T * G V R S K A I F T *
- P S N I H L F V R K V * G R K L F S R K
19261 - AATGATTAAATTTTCGTAAACGGAAGAAAATGATAAGACTATCAGGAACACTCAGAGTAC - 19320
- N D * I S L T E R K * * D Y Q E H S E Y
- M I K F R * R K E N D K T I R N T Q S T
- * L N F V N G K K M I R L S G T L R V P
19321 - CGTTTGTTCATCACAGCCTATAACTAATAAGGTGAGTTAGACGATGCACATAATGTG - 19380
- R L F I T A Y N * Y K V S L D D A H N V
- V C S S Q P I T N T R * V * T M H I M C
- F V H H S L * L I Q G E F R R C T * C A
19381 - CTACGTTAAATCCACCACGACAAACGTCTGTGGTACGTTTACTCATGGCTGTCATGAACC - 19440
- L R * I H H D K R L W Y V Y S W L S * T
- Y V K S T T T N V C G T F T H G C H E P
- T L N P P R Q T S V V R L L M A V M N L
19441 - TACGTATATTATACTACTAAAGACGACCTAAATCGGATACCTAAATGTTTGTAAACTAT - 19500
- Y V Y Y T T K D D L N R I P K C L L N Y
- T Y I I L L K T T * I G Y L N V C * T M
- R I L Y Y * R R P K S D T * M F V K L *
19501 - GAATATTGGACACCTTATGTAAATGGTCCAATGTCTCAAATCTTTACACCGAATATTAC - 19560
- E Y W T P Y V N G P M S Q I F Y T E Y Y
- N I G H L M * M V Q C L K S F T P N I T
- I L D T L C K W S N V S N L L H R I L Q
19561 - AACAAATTATTTCTGTGAAACTACCTGTGCGGCGCTTCGTGGACAAAGGTAGTAATTAT - 19620
- N N Y F L * N Y L C G R F V D K G S N Y
- T I I S C E T T C A A A S W T K V V I I
- Q L F P V K L P V R P L R G Q R * * L L
19621 - TACGACAAATGTGTTCCATCTACCATAACTACCTCTAGAAACITTTATCTGTTGTG - 19680
- Y D K C V S I Y H N Y T S R N F Y S V V
- T R N V F P S T I T T P L E T F I L L *
- R Q M C F H L P * L H L * K L L F C C E
19681 - AAGGACAATTACAACGTAAACTCGAAACCCGATTGCGATTGTAATTTGGTCACGGTCTCT - 19740
- K D N Y N V N S K P D S H C N L V T V S
- R T I T T * T R N P I R I V I W S R S L
- G Q L Q R K L E T R F A L * F G H G L *
19741 - AATTCTATGAGTTATTAAACCCACAACATATAGCGACGATTATGACATTAGACCCTGATGT - 19800
- N S M S Y * T H N Y S D D Y D I R P * C
- I L * V I K P T I A T I M T L D P D V
- F Y E L L N P Q L * R R L * H * T L M F

FIG. 5 Cont'd

19801 - TTTCTCTTCGGGGTCGTGTACATAGATGTTATCCACAGACGTGTTACTGACTGTAACGGT - 19860
- F L F G V V Y I D V I H R R V T D C N G
- F S S G S C T * M L S T D V L L T V T V
- S L R G R V H R C Y P Q T C Y * L * R F
19861 - TCTTTGGATGACTCTCACGAACAAGAAGTGAATGACAGAACAACACTACCATCTCACCTTC - 19920
- S L D D S H E Q E V N D R T N Y H L T F
- L W M T L T N K K * M T E Q T T I S P S
- F G * L S R T R S E * Q N K L P S H L P
19921 - CTGTCCATCTGGAAAAATCTTTGCGGGCATTACCACAAAATTATTGTCTTCCAAGTCAGT - 19980
- L S I W K N L C G H Y H K I I V F Q V S
- C P S G K I F A G I T T K L L S S K S V
- V H L E K S L R A L P Q N Y C L P S Q F
19981 - TTCCAGATTGTGGAAGTTCCCTGGTCGTGTTTCGATCGCAGTTACCTCAGTGTAATTAAC - 20040
- F Q I V E V S L V V F D R S Y L S V I N
- S R L W K F P W S C S I A V T S V * L T
- P D C G S F P G R V R S Q L P Q C N * P
20041 - CTCTTAGTCATTTTGTGTCAAATTGATGAAATCTTTCATCTGCCGTAATAAGTTGTCA - 20100
- L L V I F V S N * * N S F I C R N K L S
- S * S F L C Q I D E I L S S A V I S C Q
- L S H F C V K L M K F F H L P * * V V N
20101 - ACGGACTTTGGATGAAATGAGTCTCGTCTCTGAATCTCCTAAAATTCGGGTCTAGTGT - 20160
- T D F G * N E S R L * I S * N S G L V F
- R T L D E M S L V S E S P K I R V * C L
- G L W M K * V S S L N L L K F G S S V Y
20161 - ACCTTTGACTGAAAGAGCTCGAGCGATACCTACTTAAGTATGTCGTATATTTCGAGCTCC - 20220
- T F D * K S S S D T Y L S M S L Y S S S
- P L T E R A R A I P T * V C R Y I R A P
- L * L K E L E R Y L L K Y V A I F E L P
20221 - CGATACGGAAGCTTGTGTAGCAAATACCTCTAAAGTCAGTACCTGTTGAACCGCCAGAAG - 20280
- R Y G S L C S K Y L * S Q Y L L N R Q K
- D T E A C V A N T S K V S T C * T A R S
- I R K L V * Q I P L K S V P V E P P E V
20281 - TAAATTACTATCCGAATCGGTTTCGCGAGTGTCTAAGTGGTGAATTTAATCTCCTAAAAT - 20340
- * I T I R I G S R V F * V V N L I S * N
- K L L S E S V R E C S K W * I * S P K I
- N Y Y P N R F A S V L S G E F N L L K *
20341 - AGGGATACCTGTCGTGTCACTTTTAAATGAAGTATGTCTACGCGTTTGTCCAAGTAGTT - 20400
- R D T C R V T F * * S I V Y A F V Q V V
- G I P V V S L F N E V L S T R L S K * F
- G Y L S C H F L M K Y C L R V C P S S F
20401 - TTACACACACAAGACACTAACTAGAAAATGAACTACTGAAACAGCTCTATTATTTTCAGTG - 20460
- L H T Q D T N * K M N Y * N S S I I S V
- Y T H K T L T R K * T T E T A L L F Q C
- T H T R H * L E N E L L K Q L Y Y F S V
20461 - TTCTAAACAGTCACTAAAGTTTTACCAGTTCCAATGTAACTGATACGACTTTAAAGTA - 20520
- F * T V T K V F T S S N V N * Y D F K V
- S K Q S L K F S P V P M L T D T T L K *
- L N S H * S F H Q F Q C * L I R L * S K
20521 - AGTACGAAACCACATTCCTACCTGTACAACTTTGAAGATGGGTTTTGATGTTTCGTTTCAG - 20580
- S T K P H S Y L Y N F G R W V L M F V Q
- V R N H I P T C T T L E D G F * C S F S
- Y E T T F L P V Q L W K M G F D V R S V
20581 - TTCGCACCGTTGGTCCACAACGCTACGGATTGAACATGTTCTACGTTTCTTACGAAGAAC - 20640
- F A P L V H N A T D * T C S T F L T K N
- S H R W S T T L R I E H V L R F L R R T
- R T V G P Q R Y G L N M F Y V S Y E E L
20641 - TTTTCACACTGGAAGTCTTAATACCAGTTTACGACAATATGGTTTTCTTATTACTACT - 20700
- F S H W K S * Y H F Y D N M V F L I T T
- F H T G S L N T T F T T I W F S L L L L
- F T L E V L I P L L R Q Y G F P Y Y Y L

FIG. 5 Cont'd

20701 - TACAGCGTTTCATATGAGTTGACACAGTTATGAATTTATGTGAATGAAATCGACATGGGA - 20760
- Y S V S Y E L T Q L * I Y V N E I D M G
- T A F H M S * H S Y E F M * M K S T W D
- Q R F I * V D T V M N L C E * N R H G M
20761 - TGTGTACTCTCAATAAGTGAAACCACGACCGAGACTATTTCTCAACGTGGTCCATGTC - 20820
- C C T L N K * N H D R D Y F L N V V H V
- V V L S I S E T T T E T I S S T W S M S
- L Y S Q * V K P R P R L F P Q R G P C R
20821 - GACACGAGTCTGTTACCAACGGTTGACCGTGTGATGAACAGCTAAGTCTAGAATTACTGA - 20880
- D T S L L P T V D R V M N S * V * N Y *
- T R V C Y Q R L T V * * T A K S R I T E
- H E S V T N G * P C D E Q L S L E L L K
20881 - AGCAGAGGCTCGCTCTAAGATGAAATTAACCTCTGACACGTTGTATGATGCCGATTAT - 20940
- S R G C V * D E I N L * H V V M Y A D Y
- A E A A S K M K L T S D T L S C M P I I
- Q R L R L R * N * P L T R C H V C R L F
20941 - TTACCCTGGAATAATAATCGCTATACATACTGGGATCCTGGTTTGTACACTGTTTCTCT - 21000
- L P W N N N R Y T Y W D P G L Y T V F S
- Y P G I I I A I H T G I L V C T L F S L
- T L E * * S L Y I L G S W F V H C F L L
21001 - TACTGAGATTTCTTCCCAAAAAGTGAATAGACACACCTAAATATTCGTTTTTGATCGGG - 21060
- Y * D F F P K S E * T H L N I S F L I G
- T E I S S Q K V N R H T * I F R F * S G
- L R F L P K K * I D T P K Y F V F D R D
21061 - ACCCACCAAGATATCGACATTTCTATTGTCTCGTAAGAACCTTACGACTGGAAATGTTTCG - 21120
- T H Q D I D I S I V S * E P Y D W K C S
- P T K I S T F L L S R K N L T T G N V R
- P P R Y R H F Y C L V R T L R L E M F E
21121 - AATACCCGGTAAAGAGTACCACCTGTGAAAACAATGTTTACATTTACGTAGTAGTAGCC - 21180
- N T R * R V P P V E N N V Y I Y V V V A
- I P G K E Y H L S K T M F T F T * * * P
- Y P V K S T T C R K Q C L H L R S S S L
21181 - TTCGTAAAAATTAACCCGATTGATAGAACCGTTCGGCTTCCTTGTTAACTACCGATAT - 21240
- F V K I N P D * * N R S A S L F N Y R Y
- S * K L T P I D R T V R L P C L T T D M
- R K N * P R L I E P F G F L V * L P I W
21241 - GGTACGTACGATTGATGTAAAAGACCTCCTTGTGTTTAGGATAGGTCAACAGAAGGATAA - 21300
- G T Y D * C K R P P C V * D R S T E G *
- V R T I D V K D L L V F R I G Q Q K D K
- Y V R L M * K T S L C L G * V N R R I S
21301 - GTGAGAACTGTACTCGTTTAAAGGAGAATTTAATTCTCCTTGACGACATTACAGAGAAT - 21360
- V R N C T R L K E N L I L L D D I T E N
- * E T V L V * R R I * F S L T T L Q R I
- E K L Y S F K G E F N S P * R H Y R E F
21361 - TCCTCTTAGTTTAGTTACTATACTAAATAAGAGAAGACCTTTTCCATCCGAATAGTAAT - 21420
- S S * F S Y T K * E K T F F H P N S N
- P L S L V T I L N K R R P F S I R I V I
- L L V * L L Y * I R E D L F P S E * * S
21421 - CTCTTTTGTGTCTCAACACCAAAGTTCACATAAGAACAATTGTTGATTGCTTGTACA - 21480
- L F C C L N T K V H Y K N N C * F A C T
- S F V V S T P K F T I R T I V D L L V Q
- L L L S Q H Q S S L * E Q L L I C L Y K
21481 - AATAAAGAATAATAAAGAATGAGAGTGATCACCATCACTGGAACCTGGCCACGTGGTGAA - 21540
- N K R I I K N E S D H H H W N W P R G E
- I K E * * R M R V I T I T G T G H V V K
- * K N N K E * E * S P S L E L A T W * K
21541 - AACTACTACAAGTTCGAGGATTAATGTGAGTTGTATGAAGTAGATACTCCCCCAAATGA - 21600
- N Y Y K F E D * C E L Y E V D T P P K *
- T T T S S R I N V S C M K * I L P P N D
- L L Q V R G L M * V V * S R Y S P Q M I

FIG. 5 Cont'd

21601 - TAGGACTACTTTAAAAATCTAGTCTGTGAGAAATAAATTGAGTCCTAAATAAAGAAGGTA - 21660
- * D Y F K N L V C E K * I B S * I K K V
- R T T L K I * S V R N K L S P K * R R *
- G L L * K S S L * E I N * V L N K E G K
21661 - AAATAAGATTACAATGTCCCAAAGTATGATAATTAGTATGCAAACGTGTTGGGACAGTATG - 21720
- K * D Y N V P K Y D N * Y A N C W D S M
- N K I T M S Q S M I I S M Q T V G T V W
- I R L Q C P K V * * L V C K L L G Q Y G
21721 - GAAAATTCCTACCATAAATAAACGACGGTGTCTCTTAGTTTACAACAGGCACCAACCC - 21780
- E N S Y H K * N D G V S L V Y N R H Q P
- K I P T I N K T T V S L * F T T G T N P
- K F L P * I K R R C L F S L Q Q A P T Q
21781 - AAAAACCAAGATGGTACTTGTGTTTCAGTGTGAGCCACTAATAAATTGTTAAGATGAT - 21840
- K N Q D G T C C S V S A T N N N C * D D
- K T K M V L V V Q C Q P L I I I V K M I
- K P R W Y L L F S V S H * * * L L R * L
21841 - TACAACAATATGCTCGTACATTGAACTTAACACACTGTTGGGAAAGAAACGACAAAGAT - 21900
- Y N N M L V H * N L T H C W E R N D K D
- T T I C S Y I E T * H T V G K E T T K I
- Q Q Y A R T L K L N T L L G K K R Q R F
21901 - TTGGGTACCCATGTGTCTGTGTATGATACTATAAGCTATTACGTAAATTAACGTGAAAGC - 21960
- L G T H V S V Y D T I S Y Y V N * R E S
- W V P M C L C M I L * A I T * I N V K A
- G Y P C V C V * Y Y K L L R K L T * K L
21961 - TCATGTATAGACTACGGAAGCGAACTACAAAGTCTTTTCAGTCCATTAAAATTTGTGA - 22020
- S C I D Y G K A N Y K V F S V H * N L *
- H V * T T E K R T T K S F Q S I K I C E
- M Y R L R K S E L Q S L F S P L K F V N
22021 - ATGCTCTCAAACAAATTTTATTCTACCCAAAGAGATACAAATATTCCCGATAGTTG - 22080
- M L S N T N F Y F Y P K R Y K Y S R * L
- C S Q T Q I F I S T Q R D T N I P D S W
- A L K H K F L F L P K E I Q I F P I V G
22081 - GATATCTACATCAAGCACTAGATGGAAGACCAAAATTTGTGAAACTTTGGATAAAAATTCA - 22140
- D I Y I K H * M E D Q N C E T L D K N S
- I S T S S T R W K T K I V K L W I K I Q
- Y L H Q A L D G R P K L * N F G * K F N
22141 - ACGGAGAACCATAATTGTAATGTTTAAATCTCGGTAAGAATGTGCGAAAAGTGGACGAG - 22200
- T E N H N C N V * N L G K N V G K V D E
- R R T I I V M F K I S V R M S E K W T S
- G E P * L * C L K S R * E C R K S G R V
22201 - TTCTGTGAACCCCGTGCAGTCGACGTCGGATAAAACAACCGATAAATTTTCGTTGATGTA - 22260
- F C E P R A V D V G * N N R * I S V D V
- S V N P V Q S T S D K T T D K F R L M *
- L * T P C S R R R I K Q P I N F G * C K
22261 - AATACGAGTTCATACTACTTTTACCATGTTAGTGTCTACGACAATAACAAGAGTTTGTAG - 22320
- N T S S Y Y F Y H V S V Y D N * Q E F *
- I R V H T T F T M L V S T T T N K S F R
- Y E F I L L L P C * C L R Q L T R V L G
22321 - GTGAACGACTTGAGTTTACGAGACAATTCTCGAACTCTAACTGTTTCCTTAAATGGTCT - 22380
- V N D L S L R D N S R N S N C F L K W S
- * T T * V Y E T I L E T L T V S L N G L
- E R L E F T R Q F S K L * L F P * M V W
22381 - GGAGATTAAAGTCCCAACAAGGGAGTCTCTACAACACTCTAAGGGATTATAATGTTTGA - 22440
- G D * S P N K G V L Y N T L R D Y N V *
- E I K V P T R E S S T T L * G I I M F E
- R L K S Q Q Q S P L Q H S K G L * C L N
22441 - ACACAGGAAAACCTCTCCAAAAATTACGATGATTTAAGGGAAGACAGATACGTACCCTCT - 22500
- T Q E N L S K N Y D D L R E D R Y V P S
- H R K T S P K I T M I * G K T D T Y P L
- T G K P L Q K L R * F K G R Q I R T L S

FIG. 5 Cont'd

22501 - CTTTTTTTTTAAAGATTAACACAACGACTAATGAGACACGAGATGTTGAGTTGTAAAAAA - 22560
- L F F K D * H N D * * D T R C * V V K K
- F F L K I N T T T N E T R D V E L * K K
- F F * R L T Q R L M R H E M L S C K K S
22561 - GTTGGAAATTCACGATACCGCAAAGACGGTGATTCAACTTACTAGAAACGAAGAGGTTAC - 22620
- V G N S R Y R K D G D S T Y * K R R G Y
- L E I H D T A K T V I Q L T R N E E V T
- W K F T I P Q R R * F N L L E T K R L Q
22621 - AGATACGTCTAAGAAAACATCAGTTCCTCTACTACATTCTGTTTATCGCGGTCTGTTT - 22680
- R Y V * E N I S S L Y Y I L F I A V L F
- D T S K K T S V P S T T F C L S R S C L
- I R L R K H Q F P L L H S V Y R G P V *
22681 - GACCACAATAACGACTAATATTAATTTAACGGTCTACTAAAGTACCCAACACAGGAAC - 22740
- D H N N D * Y * Y L T V Y * S T Q H R N
- T T I T T N I N I * R S T K V P N T G T
- P Q * R L I L I F N G L L K Y P T Q E R
22741 - GAACCTTATGATCCTTGTAACTACGATGAAGTTGACCATTAAATATTAATATTATATCCA - 22800
- E P Y D P C N Y D E V D H * Y * Y L Y P
- N L M I L V T T M K L T I N I N I Y I H
- T L * S L * L R * S * P L I L I F I S I
22801 - TAGAATCTGTACCGTTTGAATCCGGGAAACTCTCTCTGTATAGATTACCGGAAAGAGGG - 22860
- * N L Y R S N P G N S L C I D Y T E R G
- R I C T V R I R E T L S V * I T R K E G
- E S V P F E S G K L S L Y R L H G K R G
22861 - GACTACCGTTTGAACGTGGGGTGGACGAGAATTAACAATAACCGGTAATTTACTAATAC - 22920
- D Y R L E R G V D E N * Q * P V I Y * Y
- T T V W N V G W T R I N N N R * F T N T
- L P F G T W G G R E L T I T G N L I P
22921 - CAAAAATGTGGTGATGACCGTAACCGATGGTTGGAATGTCTCAACATCATGAAAGAAAAC - 22980
- Q K C G D D R N R W L E C L N I M K E N
- K N V V M T V T D G W N V S T S * K K T
- K M W * * P * P M V G M S Q H H E R K L
22981 - TTGAAAATTTACGTGGCCGGTGCCAAACACCTGGTTTAAATAGGTGACTGGAATAATCT - 23040
- L K I Y V A G A K H L V L I G D W N N S
- * K F T W P V P N T W F * * V T G I I L
- E N L R G R C Q T P G F N R * L E * F L
23041 - TGGTCACACAGTTAAAATTAAAATTACCTGAGTGACCATGACCACACAATTGAGGAAGAA - 23100
- W S H S * N * N Y L S D H D H T I E E E
- G H T V K I K I T * V T M T T Q L R K K
- V T Q L K L K L P E * P * P H N * G R S
23101 - GTTCTCTAAAGTTGGTAAAGTTGTTAAACCGGCACTACAAAGACTAAAGTGACTAAGGC - 23160
- V S L K L V K L L N R H Y K D * S D * G
- F L * S W * S C * T G T T K T K V T K A
- F S K V G K V V K P A L Q R L K * L R Q
23161 - AAGCTCTAGGATTTGTAGACTTTATAATCTGTAAGTGGAACGAGAAAACCCACATT - 23220
- K L * D F V D F I I C K V E R E N P H I
- S S R I L * T L * S V K W N E K T P T F
- A L G F C R L Y N L * S G T R K P P H S
23221 - CACATTAATGTGGACCTTGTTTACGAAGTAGACTTCAACGACAAGATATAGTTCTACAAT - 23280
- H I N V D L V Y E V D F N D K I * F Y N
- T L M W T L F T K * T S T T R Y S S T I
- H * C G P C L R S R L Q R Q D I V L Q L
23281 - TGACGTGACTACAAAGATGTCGTTAAGTACGTCTAGTTGAGTGTGGTGAACCGCGTATA - 23340
- * R D Y K D V V K Y V * L S V V E P R I
- D V T T K M S L S T S S * V W S N R V Y
- T * L Q R C R * V R L V E C G R T A Y I
23341 - TAAGATGACCTTTGTTACATAAGGTCTGAGTTCGTCCGACAGAAATATCCTCGACTCGTAC - 23400
- * D D L C Y I R S E F V R Q N I L D S Y
- K M T F V T * G L S S S D R I S S T R T
- R * P L L H K V * V R P T E Y P R L V Q

FIG. 5 Cont'd

23401 - AGCTGTGAAGAATACTCACGCTGTAAGGATAACCTCGACCGTAAACACGATCAATGGTAT - 23460
- S C E E Y S R C K D N L D R K H D Q W Y
- A V K N T H A V R I T S T V N T I N G M
- L * R I L T L * G * P R P * T R S M V C
23461 - GTCAAAGAAATAATGCATCATGATCGGTTTTAGATAACACCGAATATGATACAGAAATC - 23520
- V K E I M H H D R F L D N T E Y D T E I
- S K K * C I M I G F * I T P N M I Q K S
- Q R N N A S * S V F R * H R I * Y R N P
23521 - CACGACTATCAAGTTAACGAATGAGATTATTGTGGTAACGATATGGATGATTGAAAAGTT - 23580
- H D Y Q V N E * D Y C G N D M D D * K V
- T T I K L T N E I I V V T I W M I E K L
- R L S S * R M R L L W * R Y G * L K S *
23581 - AATCGTAATGATGTCTTCATTACGGACAAAGATACCGATTTTGGAGGCATCTAACATTAT - 23640
- N R N D V F I T D K D T D F G G I * H Y
- I V M M S S L R T K I P I L E A S N I I
- S * * C L H Y G Q R Y R F W R H L T L Y
23641 - ACATGTAGACGCCTCTAAGATGACTTACACGATTAAACGAAGAGGTTATACCATCGAAAA - 23700
- T C R R L * D D L H D * T K R L Y H R K
- H V D A S K M T Y T I K R R G Y T I E N
- M * T P L R * L T R L N E E V I P S K T
23701 - CGTGTGTTGATTTAGCACGTGAGAGTCCATAACGACGACTTGTCTAGCGTTGTGTGCAC - 23760
- R V L I * H V R V H N D D L S * R C V H
- V C * F S T * E S I T T T C P S V V C T
- C V D L A R E S P * R R L V L A L C A L
23761 - TTCACAAGCGAGTTCAGTTTGTTCATGTTTGGGGTTGAAACTTTATAAAACCACCAA - 23820
- F T S E F S L F T C F G V E T L * N H Q
- S Q A S S V C L H V L G L K L Y K T T K
- H K R V Q F V Y M F W G * N F I K P P K
23821 - AATTAAAAAGTGTTTATAATGGACTGGGAGATTTCGGTTGATTCTCCAGAAAAAATCTCC - 23880
- N * K V F I M D W E I S V D S P E N N S
- I K K C L * W T G R F R L I L Q K I T P
- L K S V Y N G L G D F G * F S R K * L L
23881 - TGAACGAGAAATTATTCACCTGTGAGCGACTACGACCGAAGTACTTCGTTATACCGCTTA - 23940
- * T R N Y S T V S D Y D R S T S L Y R L
- E R E I I P L * A T T T E V L R Y T A Y
- N E K L F H C E R L R P K Y F V I P L T
23941 - CGGATCCACTATAATTACGATCTCTAGAGTAAACACGCGTCTTCAAGTTACCTGAATGTC - 24000
- R I H Y N Y D L * S K H A S S S Y L N V
- G S T I I T I S R V N T R L Q V T * M S
- D P L * L R S L E * T R V F K L P E C H
24001 - ACAACGGTGGAGACGAGTGACTACTATACTAACGACGGATGTGACGACGAGATCAATCAC - 24060
- T T V E T S D Y Y T N D G C D D E I N H
- Q R W R R V T T I L T T D V T T R S I T
- N G G D E * L L Y * R R M * R R D Q S P
24061 - CATGACGGTGACGACCTACCTGTAAACCACGACCGGACGAGAAGTTTATGGAAAACGAT - 24120
- H D G D D L P V N H D R D E K F M E N D
- M T V T T Y L * T T T A T R S L W K T I
- R R * R P T C K P R P R E V Y G K R Y
24121 - ACGTTTACCGTATATCCAAGTTACCGTAACCTCAATGGGTTTTACAAGAGATACTCTTGG - 24180
- T F T V Y P S Y R N L N G F Y K R Y S W
- R L P Y I Q V T V T S M G F T R D T L G
- V Y R I S K L P * P Q W V L Q E I L L V
24181 - TTTTGTGTTAGCGGTTGGTTAAATTGTTCCGCTAATCAGTTTAAAGTTCTTAGTGAATGTT - 24240
- F L F S G W L N C S A N Q F K F L V N V
- F C L A V G * I V P L I S L S * * M L
- F V * R L V K L F R * S V * V L S E C C
24241 - GTTGTAGTTGACGTAACCCGTTTCGACGTTCTGCAACAATTGGTCTTACGAGTTCGTAATT - 24300
- V V V D V T R S T F C N N W S Y E F V I
- L * L T * P V R R S A T I G L T S S * F
- C S * R N P F D V L Q Q L V L R V R N L

FIG. 5 Cont'd

24301 - TGTGTGAACAATTTGTTGAATCGAGATTAACCACGTTAAAGTTCACACGATTTACTAT - 24360
- C V N N L L N R D * N H V K V H T I Y Y
- V * T I C * I E I K T T L K F T R F T I
- C E Q F V E S R L K P R * S S H D L L *
24361 - AGGAAAGCGCTGAACATTTTCAGCTCCGCTCCATGTTTAACTGTCCAATTAATGTCCGT - 24420
- R K A L N Y F S S A S M F N C P I N V R
- G K R * T I S A P P P C L T V Q L M S V
- E S A E L F Q L R L H V * L S N * C P S
24421 - CTGAAGTTTCGGAAGTTTGGATACATTGTGTTGTTGATTAGTCCCGACGACTTTAGTCCC - 24480
- L K F R K F G Y I V L L I S P D D F S P
- * S F G S L D T L C C * L V P T T L V P
- E V S E V W I H C V V D * S R R L * S R
24481 - GAAGACGATTAGAACGACGATGATTTTACAGACTCACACAAGAACCTGTTAGTTTTTCTC - 24540
- E D D * N D D D F T D S H K N L L V F L
- K T I R T T M I L Q T H T R T C * F F S
- R R L E R R * F Y R L T Q E P V S F S Q
24541 - AACTGAAAACACCTTTCCCGATGGTGAATACAGGAAGGGTGTTCGTCGGGGCGTACCAC - 24600
- N * K H L S R W W N T G R V F V G A Y H
- T E N T F P D G G I Q E G C S S G R T T
- L K T P F P M V E Y R K G V R R G V P Q
24601 - AACAGAAGGATGTACAGTGCATACACGGTAGGGTCTCTCTTGAAGTGGTGTGCGGGTC - 24660
- N R R M Y S A Y T V G S S P * S G V A V
- T E G C T V H T R * G P L L E V V S R S
- Q K D V Q C I H G R V L S L K W C R G R
24661 - GTTAAACAGTACTTCCGTTTCGTATGAAGGGAGCACTTCCACAAAACACAAATTACCGT - 24720
- V K Q Y F R F V * R E H F H K N T N Y R
- L N S T S V S Y E G S T S T K T Q I T V
- * T V L P F R M K G A L P Q K H K L P *
24721 - GAAGAACCAATAATGTGTCTCCTTGAAGAAAAGAGGTGTTTATTAATGATGTCTGTTAT - 24780
- E E P N N V S P * R K E V F I N D V C Y
- K N Q I M C L L E E K R C L L M M S V M
- R T K * C V S L K K R G V Y * * C L L C
24781 - GTAAACAGAGTCTTTAACACTACAGCAATAACCGTAGTAATTGTTGTGTCAAATACTAG - 24840
- V N R V L * H Y S N N R S N C C V K Y *
- * T E S F N T T A I T V V I V V S N T R
- K Q S P L T L Q Q * P * * L L C Q I L G
24841 - GAGAGTGTGGACTCGAACTGAGTAAGTTTCTTCTCGACCTGTTTCATGAAGTTTTTAGTAT - 24900
- E T L D S N * V S F F S T C S * S F * Y
- R R W T R T E * V S S R P V H E V F S M
- D V G L E L S K F L L D L F M K F L V C
24901 - GTAGTGGTCTACAACCTAGAACCGCTGTAAAGTCCGTAATTGCGAAGACAGCAGTTGTAAG - 24960
- V V V Y N * N R C K V R N C E D S S C K
- * W S T T R T A V K S V I A K T A V V S
- S G L Q L E P L * S P * L R R Q Q L * V
24961 - TTTTCTTTAACTGGCGGAGTTACTCCAGCGATTTTTAAATTTACTTAGTGAGTAAGTGG - 25020
- F F F N W R S Y S S D F * I Y L V S N W
- F S L T G G V T P A I F K F T * * V T G
- F L * L A E L L Q R F L N L L S E * L E
25021 - AAGTTCTTAACCCTTTTATACTCGTTATATAATTTACCGGAACCATACAAACCGAGCCGA - 25080
- K F L T L L Y S L Y N L P E P Y K P S R
- S S * P F Y T R Y I I Y R N H T N R A E
- V L N P F I L V I * F T G T I Q T E P K
25081 - AGTAACGACCTGATTACGGTAGCAGTACCAATGTTAGAACGAAACAACGTACTGATCAA - 25140
- S N D L I N G S S T N V R T K Q R T D Q
- V T T * L T V A V P M L E R N N V L I N
- * R P D * R * Q Y Q C * N E T T Y * S T
25141 - CAACGTCAACGAGTTCCACGTACGAGAACCAAGAACGACGTTCAACTACTCCTAC - 25200
- Q R Q R S S H V R E H Q E R R S N Y S Y
- N V N G V P T Y E N T K N D V Q T T P T
- T S T E F P R T R T P R T T F K L L L L

FIG. 5 Cont'd

25201 - TGAGACTCGGTCAAGAGTTCCACAGTTTAATGTAATGTGTATTGCTTGAATACCTAAA - 25260
- * D S V K S S H S L M * C V F A * I P K
- E T R S R V P T V * C N V Y L L E Y L N
- R L G Q E F P Q F N V M C I C L N T * T
25261 - CAAATACTCTAAAAATGAGAACCTAGTTAATGACGTGTCGGTCATTTTAACTGTTACG - 25320
- Q I L * K M R T * L M T C R S F L T V T
- K Y S K K * E P S * * R V G H F * L L R
- N T L K N E N L V N D V S V I F N C Y E
25321 - AAGAGGACGTTTCATGACAAGTACGATGTCGTTGCTATGGCGATGTTCCGAGTGAGGGAAA - 25380
- K R T F M T S T M S L L W R C S E * G K
- R G R S * Q V R C R C Y G D V R S E G K
- E D V H D K Y D V V A M A M F G V R E S
25381 - GCCTACCGAACAATAACCGCAACGTAAAGAACGACAAAAAGTCTCGCGATGGTTTTATTA - 25440
- A Y R T I T A T * R T T K S L A M V L L
- P T E Q * P Q R K E R Q K V S R W F Y *
- L P N N N R N V K N D K K S R D G F I N
25441 - ACGCGAGTTATTTTCTACCGTCGATCGGGAAATATTTCCGAAGGTCAAGTAAACGTTAAA - 25500
- T R V I F Y R R S G N I P E G Q V N V K
- R E L F S T V D R E I F P K V K * T L N
- A S Y F L P S I G K Y S R R S S K R * M
25501 - TGACGACGATAAACAAATGGTAGATAAGTGTAGAAAACGAACAGCGACGTCCATACCTCCG - 25560
- * R R * T M V D K C R K R T A T S I P P
- D D D K Q W * I S V E N E Q R R P Y L R
- T T I N N G R * V * K T N S D V H T S A
25561 - CGTTAAAAACATGGAGATACGGAACATATATAAAGATGTTACGTAGTTGCGTACATCTTA - 25620
- R * K H G D T E L Y K R C Y V V A Y I L
- V K N M E I R N Y I K D V T * L R T S *
- L K T W R Y G T I * K M L R S C V H L N
25621 - ATAATACTCTACAACCGAAACAACCTTCACGTTTAGGTTCTTGGGTAATGAAATACTACG - 25680
- I I L Y N R N N L H V * V L G * * N T T
- * Y S T T E T T F T F R F L G N E I L R
- N T L Q P K Q P S R L G S W V M K Y Y G
25681 - GTTGATGAAACAAACGACCGTGTGTGTATTGATACTGATGACATATGGTATATTGTCACA - 25740
- V D E T N D R V C I D T D D I W Y I V T
- L M K Q T T V C V L I L M T Y G I L S Q
- * * N K R P C V Y * Y * * H M V Y C H S
25741 - GTGTCTATGTTAACAGCAATGACTTCCACTGCCGTAAAGTTGTGGTTTTGAGTTTCTTCT - 25800
- V S M L T A M T S T A V K L W F * V S S
- C L C * Q Q * L P L P * S C G F E F L L
- V Y V N S N D F H C R K V V V L S F F *
25801 - GATGGTTTTAACCAACAATAAGACTCCTATCCGTGAGTCCACAATTTCTGATACAGCAACA - 25860
- D G L T T N K T P I R E S T I S D T A T
- M V * P P I R L L S V S P Q F L I Q Q H
- W F N H Q * D S Y P * V H N F * Y S N M
25861 - TGTACCGATAAAGTGGCTTCAAATGATGGTCGAACTCAGATGTGTTAATGATGTCTGTG - 25920
- C T D K V A S N D G R T Q M C L M M S V
- V P I K W L Q M M V E L R C V * * C L *
- Y R * S G F K * W S N S D V F N D V C D
25921 - ACCATAACTTTTACGATGTAAGAAGTAGAAATTGTTTGAACAATTTCTGGGTGGCTTACA - 25980
- T I T F T M * E V E I V R T I S G W L T
- P * L L R C K K * K L F E Q F L G G L H
- H N F Y D V R S R N C S N N F W V A Y T
25981 - CGTTTATGTGTGTTAGCTGCCGAGAAGTCCTCAACGATTAGGTCGTTACCTAGGTTAAAT - 26040
- R L C V L A A E K S S T I R S L P R L N
- V Y V C * L P R S P Q R L G R Y L G * I
- F M C V S C R E V L N D * V V T * V K Y
26041 - ACTACTCGGCTGCTGCTGATGATCGCACGGAAACATTCGTGTTCTTCACTCATGCTTGA - 26100
- T T R L L L M I A R K H S C S F T H A *
- L L G C C * * S H G N I R V L S L M L E
- Y S A A A D D R T E T F V F F H S C L N

FIG. 5 Cont'd

26101 - ATACATGAGTAAGCAAAGCCTTCTTTGTCCATGCAATTATCAATTATCGCATGAAGAAAA - 26160
- I H E * A K P S L S M Q L S I I A * R K
- Y M S K Q S L L C P C N Y Q L S H E E K
- T * V S K A F F V H A I I N Y R M K K K
26161 - AGAACGAAAGCACCATAAGAACGATCAGTGTGATCGGTAGGAATGACGCGAAGCTAACAC - 26220
- R T K A P * E R S V * S V G M T R S * H
- E R K H H K N D Q C D R * E * R E A N T
- N E S T I R T I S V I G R N D A K L T H
26221 - ACGCATGACGACGTTATAACAATTGCACTCAAATCATTGTTGGTTGCCAAATGCAGATGAG - 26280
- T H D D V I T I A L K S F W L P N A D E
- R M T T L * Q L H S N H F G C Q M Q M S
- A * R R Y N N C T Q I I L V A K C R * A
26281 - CGCACAATTTTAGACTTGAGAAGACTTCCTCAAGCACTAGAAGACCAGATTGCTTGAT - 26340
- R T I F R L E K T S S R T R R P D L L D
- A Q F L D L R R L P Q G L E D Q I C L I
- H N F * T * E D F L K D * K T R F A * L
26341 - TGATAATAATAATAAGACAAACCTTGAAATTGTAACGAATAGTACCGTCTGTTGCCATGA - 26400
- * * * * D K P * N C N E * Y R L L P *
- D N N N K T N L E I V T N S T V C C H D
- I I I I R Q T L K L * R I V P S V A M I
26401 - TAATGGCAACTCCTCGAATTTGTTGAGGACCTTGTTACCTTGGATCATTATCCAAAGGAT - 26460
- * W Q L L E F V E D L V T L D H Y P K D
- N G N S S N L R T L L P W I I I Q R I
- M A T P R I C * G P C Y L G S L S K G *
26461 - AAGGATCGGACCTAATACAATGATGTTAAACGGATAAGATTAGCCTTGTCAAAAACATG - 26520
- K D R T * Y N D V K R I R L A L S K N M
- R I G P N T M M L N G * D * P C P K T C
- G S D L I Q * C * T D K I S L V Q K H V
26521 - TATTATTTTGAACAAAAGGAGACCGAGAACCGGTTCATTGTGAACGAACAAACACGAA - 26580
- Y Y F E Q K E T E N T G H C E R T K H E
- I I S N K R R P R T P V I V N E Q N T N
- L F R T K G D R E H R S L * T N K T R T
26581 - CGACGACAGATGTCTTAATTAACCCACTGACCGCCCTAACGCTAACGTTACCGAACATAA - 26640
- R R Q M S * L T H * P P * R * R Y R T *
- D D R C L N * P T D R P N A N V T E H N
- T T D V L I N P L T A L T L T L P N I T
26641 - CATCCGAACCTACCCGAATCGATGAAGCAACGAAGGAGTCCGACAAACGAGCATGGGCG - 26700
- H P N Y T E S M K Q R R K S D K R A W A
- I R T T P N R * S N E G S P T N E H G R
- S E L H R I D E A T K E V R Q T S M G E
26701 - AGTTACACCAGTAAGTTGGGTCTTTGTTTGAAGAAGATTACACGGAGAGGCCCCCTGT - 26760
- S Y T S K L G L C L * E E L H G E A P C
- V T P V S W V F V C K K S Y T E R P P V
- L H Q * V G S L F V R R V T R R G P L L
26761 - TAACACTGGTCTGGCGAGTACCTTTCACTTGAACAGTAACCACGACACTAGTAAGCACCA - 26820
- * H W S G E Y L S L E Q * P R H * * A P
- N T G L A S T F H L N S N H D T S K H Q
- T L V W R V P F T * T V T T T L V S T S
26821 - GTGAACGCTTACCGCCTGTGAGGGATCCCGGACACTGTAATTCTGACGGTTTCTC - 26880
- V N A Y R P V R D P A T L * F L D G F L
- * T L T G L * G I P R H C N S W T V F S
- E R L P A C E G S R D T V I P G R F S L
26881 - TAGTGACACCGATGTAGTGCTTGCAGAAAGATAATGTTAATCCTCGCAGCGTCGCACAT - 26940
- * * H R C S A C E R I M F N P R S V A H
- S D T D V V L A K E * C L I L A A S H I
- V T P M * C L R K N N V * S S Q R R T S
26941 - CCGTGACTAAGTCCAAACGACGTATGTTGGCGATGCATAACCTTTGATATTTAATTTA - 27000
- P * L S P K R R M L A M A * P L I F N L
- R D * V Q N D V C W R W H N L * Y L I Y
- V T K S K T T Y V G D G I T F D I * F M

FIG. 5 Cont'd

27001 - TGTCTGGTGGCGCCATCGTTGCTGTTATAACGAAACGATCATGTCATTCACTGTTGTCTA - 27060
- C L V R P S L L L * R N D H V I H C C L
- V W C G H R C C Y N E T I M S F T V V Y
- S G A A I V A V I T K R S C H S L L S T
27061 - CAAAGTAGAACAACTGAAGGTCCAATGTTATCGTCTCTATAACTAATAGTAATACTCCTG - 27120
- Q S R T T E G P M L S S L * L I V I L L
- K V E Q L K V Q C Y R L Y N * * * Y S *
- K * N N * R S N V I V S I T N S N T P E
27121 - AAAGTCCTAACGATAAACCTTAGAACTGCAATATTATTCAAGTTATCACTCTGTTAATAA - 27180
- K V L T I N L R T A I L F K L S L C * *
- K S * R * T L E L Q Y Y S S Y H S V N K
- S P N D K P * N C N I I Q V I T L L I N
27181 - ATTCGGAGATTGATTCTTCTTAATAAGCCTCAATCTACTACTTCTTGGATACCTCAATCT - 27240
- I R R L I L L N K P Q S T T S W I P Q S
- F G D * F F L I S L N L L L L G Y L N L
- S E I D S S * * A S I Y Y F L D T S I *
27241 - AATAGTATTTTGTCTTGTACTTTTAATAAGAGAAGGACTGTAACTAACATAAATGTAGAA - 27300
- N R Y F A C T F N K R R T V T N I N V E
- I G I L L V L L I R E G L * L T * M * N
- * V F C L Y F * * E K D C N * H K C R T
27301 - CGCTCGATATAGTAGTCTCTCACACAATCTCCATGCTGACATGATGATTTTCTTGGAA - 27360
- R S I * * * S S H N L H A D M M I F L E
- A R Y S D S P H T I S M L T * * F S W N
- L D I V I V L T Q S P C * H D D F L G T
27361 - CGGGTAGTCCTTGTATGCTCCCGTTAAGTGGTAAAGTGGGAGAACGACTGTTATTTAAAC - 27420
- R V V L V C S R * V V K W E N D C Y L N
- G * S L Y A P V K W * S G R T T V I * T
- G S P C M L P L S G K V G E R L L F K R
27421 - GTGATTGAACGTGATCGTGTGTGAAACGAAACGAAACGACTGCCATGAGCTGTATGGA - 27480
- V I E R D R V * N E N E H D C H E L Y G
- * L N V I V C E T K T N T T A M S C M D
- D * T * S C V K R K R T R L P * A V W I
27481 - TAGTCGACGCACGTTCTAGTCAAAGTGGTTTGAAGTAGTCTGTTCTCTCTCCAAGTTG - 27540
- * S T H V L V K V V L K S S L F S S K L
- S R R T F * S K W F * K V V C S P P S C
- V D A R S S Q S G F E K * S V L L Q V V
27541 - TTCTCGAGATGAGCGGTGAAAAAGAGTAACAACGACGAGATCATAAAAATTATGAAACGA - 27600
- F S R * A V K K S N N D E I I K I M K R
- S R D E R * K R V T T T R S * K L * N E
- L E M S G E K E * Q R R D H K N Y E T K
27601 - AGTGGTAATTCTCTTCTGCTTACTTACTCGAGTGAAATTAAGTGAAGATAAACACGAA - 27660
- S G N S L S V L L T R V K L T E D K H E
- V V I L F L S Y L L E * N * L K I N T K
- W * F S F C L T Y S S E I N * R * T R K
27661 - AAATCGGAAAGACGATAAGGAACAAAATTATTACGAATAATATAAAACAAAAGTGAGCT - 27720
- K S E R R * G T K L L R I I * N Q K * A
- N R K D D K E Q N Y Y E * Y K T K S E L
- I G K T I R K I Y T N N I K P K V S F
27721 - TTAGGTCTAGATCTTCTTGGAACATGGTTTCAGATTGCTTGTACTTTGAAGAGTAACA - 27780
- L G P R S S W N M V S D L L V L * R V T
- * V L D L L G T W F Q I C L Y F E E * Q
- R S * I F L E H G F R F A C T L K S N K
27781 - AAAGTGAACATAAAGAGATACGTCAACGTATGCGTGACATCATGTCGCGACAGTAGATT - 27840
- K L N I K R Y V N V C V T S C R D T * I
- N * T * R D T S T Y A * H H V A T R R L
- T E H K E I R Q R M R D I M S R H V D Y
27841 - ATTTGGAGTACACGAACTTCTAGGAACATTCCATGTTGTGATCCCCATTATGAATATCGT - 27900
- I W S T R T S R N I P C C D P H Y E Y R
- F G V H E L L G T F H V V I P I M N I V
- L E Y T N F * E H S M L * S P L * I S *

FIG. 5 Cont'd

27901 - GACGAACCGAAACACGAGATCCTTTCCAAAATGGAAAAGTATCTACCGTGTGATACCAAG - 27960
- D E P K H E I L S K M E K Y L P C D T K
- T N R N T R S F P K W K S I Y R V I P S
- R T E T R D P F Q N G K V S T V * Y Q V
27961 - TTTGTACGTGTGGATTACAATGATAGTTGACAGTTCTAGGTCGACCACCACGCGAATATC - 28020
- F V R V D Y N D S * Q F * V D H H A N I
- L Y V W I T M I V D S S R S T T T R I S
- C T C G L Q * * L T V L G R P P R E Y R
28021 - GATCCACAACCATGGAAGTACTTCCAGTGGTTTGACGACGTAAATCTCTGCATGAACAAC - 28080
- D P Q P W K Y F Q W F D D V N L C M N N
- I H N H G S T S S G L T T * I S A * T T
- S T M E V L P V * R R K S L H E Q Q
28081 - AAAATTTATTTGCTTGTGTTTAAATTTTACAGACTATTACCTGGGGTTAGTTGGTTGCATCA - 28140
- K I Y L L V * F Y R L L P G V S L V A S
- K F I C L F N F T D Y Y L G L V W L H H
- N L F A C L I L Q T I T W G * F G C I T
28141 - CGGGGGCGTAATGTAAACCACCTGGGTGTCTAAGTTGACTGTTATTGGTCTTACCTCCT - 28200
- R G A * C K P P G C L S * L L L V L P P
- G G R N V N H L G V * V D C Y W S Y L L
- G G V M * T T W V S K L T V I G L T S C
28201 - GCCTTACCCCGTTCCGGTTTTGTCGCGGCTGGGGTTCCAAATGGGTTATTATGACGCAGA - 28260
- A L P R S G F V A A G V P N G L L * R R
- R Y P V P V L S R L G F Q M G Y Y D A E
- V T P F R F C R G W G S K W V I M T Q N
28261 - ACCAAGTGTGAGAGTGAGTCGTACCGTTCCCTCCTTGAATCTAAGGGAGCTCCGGTCCCG - 28320
- T K C R E * V V P F L L E S K G A P V P
- P S V E S E S Y R S S L N L R E L R S R
- Q V S R V S R T V P P * I * G S S G P A
28321 - CAAGGTTAGTTGTGTTATCACCAGGTCTACTGGTTAACCAGATGATGGCTTCTCGATGG - 28380
- Q G * L W L S P G L L V * P M M A S R W
- K V S C G Y H Q V Y W F N R * W L L D G
- R L V V V I T R S T G L T D D G F S M G
28381 - GCTGCTCAAGCACCACCACTGCCGTTTTACTTTCTCGAGTCGGGGTCTACCATGAAGATA - 28440
- A A Q A P P L P F Y F L E S G S T M K I
- L L K H H H C R F T F S S R G L P * R *
- C S S T T T A V L L S R V G V Y H E D N
28441 - ATGGATCCTTGACCGGGTCTTCGAAGTGAAGGGATGCCGCGATTGTTTCTCCGTAGCAT - 28500
- M D P * P G L R S E G M P R L F L P * H
- W I L D R V F E V K G C R D C F F R S I
- G S L T G S S K * R D A A I V S S V A Y
28501 - ACCCAACGTTGACTCCCTCGGAACCTTATGTGGTTTCTGGTGTAAACCGTGGGCGTTAGGA - 28560
- T Q R * L P R N L C G F L V * P W A L G
- P N V D S L G T Y V G F W C N R G R * D
- P T L T P S E L M W V S G V T V G V R I
28561 - TTATTGTTACGACGGTGGCAGATGTTGAAGGAGTTCCTTGTGTGAACGGTTTCCGAAG - 28620
- L L L R R W H D V E G V P C C N G F P K
- Y C Y D G G T M L K E F L V V T V F R R
- I V T T V A R C * R S S L L * R F S E D
28621 - ATGCGTCTCCCTTCGTCTCCGCCGTGAGTTCGGAGAAGAGCGAGGAGTAGTGCATCAGCG - 28680
- M R L P S S P P S V R R R A R S S A S A
- C V S L R L R R Q F G E E R G V V H Q R
- A S P F V S A V S S E K S E E * C I S A
28681 - CCATTAAGTTCTTTAAGTTGAGGACCGTCATCCCCTTTAAGAGGACGAGCTTACCGA - 28740
- P L S S L S * G P S S S P L R G R A Y R
- H * V L * V E D R R H P L * E D E L T D
- I K F F K L R T V V I P P K R T S L P I
28741 - TCGCCTCCACCACCTTGACGGGAGCGGATAACGACGATCTGTCTAACTGGTCAACTC - 28800
- S P P P L * R E R D N D D L S N L V E L
- R L H H F D G S A I T T I C L T W S N S
- A S T T L T G A R * R R S V * L G R T L

FIG. 5 Cont'd

28801 - TCGTTTCAAAGACCATTTCGGTTGTTGTTGTTCCGGTTTGACAGTGATTCTTTAGACGA - 28860
- S F Q R P F P V V V P V * Q * F F R R
- R F K D H F R L L L F R F D S D S L D D
- V S K T I S G C C C S G L T V I L * T T
28861 - CGACTCCGTAGATTTTTCGGAGCGGTTTTGTCATGACGGTGTTCATGTTGCAGTGA - 28920
- R L R R P F G A V F A * R C F V M L Q *
- D S V D F S E R F L H D G V L S C C S E
- T P * I F R S G F C M T V F C H V A V S
28921 - GTTCGTAAACCTCTGCACCAGGTCTTGTGGGTTTCCTTAAAGCCCTGGTTCTGGAT - 28980
- V R K P S A P G L V W V P L K P L V L D
- F V N P L H Q V L F G F L * S P W F W I
- S * T L C T R S C L G S F K A P G S G L
28981 - TAGTCTGTTCCCTTGACTAATGTTTGTAAACGGCGTTTAAACGTGTTAAACGAGGTTACACGG - 29040
- * S V P * L M F V T G V * R V K R G S R
- S L F L D * C L * P A F N V L N E V H G
- V C S L T N V C N R R L T C * T R F T E
29041 - AGACGTAAGAAACCTTACAGTGCGTAACCGTACCTTCAGTGTGGAAGCCCTTGTACCGAC - 29100
- R R K K P Y S A * P Y L Q C G S P C T D
- D V R N L T V R N R T F S V E A L V P T
- T * E T L Q C V T V P S V W K P L Y R L
29101 - TGAATAGTACCTCGGTAATTTAACTACTGTTTCTAGGTGTTAAGTTCTGTGTCAGTAT - 29160
- * I V P R * F N L L F L G V K F L L Q Y
- E * Y L G N L T Y C F * V L S F C C S M
- N S T S V I * P T V S R C * V S V A V *
29161 - GACGACTTGTTTCGTGTAAGTGCATGTTTGTAAAGGTTGGTGTCTCGGATTTTCTCG - 29220
- D D L F V * L R M F C K G G C L G F F L
- T T C S C N C V C F V R V V V S D F S C
- R L V R V T A Y V L * G W L S R I F P V
29221 - TTTTCTTTTCTGACTACTTCGAGTCGGAAACGGCGTCTCTGTTTCTTCGTCGGGTGA - 29280
- F F F F * L L R V G N G V S V F F V G *
- F S F S D Y F E S E T A S L F S S S G D
- F L F L T T S S R K R R L C F L R R V T
29281 - CACTGAGAAGAAGGACGCCGACTGTACCTACTAAAGAGGTCTGTTGAAGTTTAAAGGTAC - 29340
- H * E E G R R L Y L L K R S V E V L R Y
- T E K K D A D C T Y * R G L L K F * G T
- L R R R T P T V P T K E V C * S F K V L
29341 - TCACCTCGAAGACGACTAAGTTGAGTCCGTATTTGTGAGTACTACTGGTGTGTTCCGTCT - 29400
- S P R R R L L S * V R I C E Y Y W C V P S
- H L E D D * V E S V F V S T T G V F R L
- T S K T T K L S P Y L * V L L V C S V Y
29401 - ACCCGATACATTGCAAAAGCGTTAAGGCAATGCTATGTATCAGATGAGAACACGTCTT - 29460
- T R Y I C K S V K A N A M Y Q M R T R L
- P D T F A K A L R Q M L C I R * E H V L
- P I H L Q K R * G K C Y V S D E N T S Y
29461 - ACTTAAGAGCATGATTTGTCGTGTTTCATCCAAATCAATTGAAATTAGAGTGTATCGTTA - 29520
- T * E H * F V V F I Q I N * N * S V S L
- L K S I D L S C S S S K S I E I R V Y R *
- L R A L I C R V H P N Q L K L E C I V R
29521 - GAAATTAGTTACACATTGTAATCCCTCCTGAACCTTCTCGGTGGTGTAAAAGTAGCTCCG - 29580
- E I S Y T L * S L L N F L G G V K V A P
- K L V T H C N P S * T F S V V * K * L R
- N * L H I V I P P E L S R W C K S S S G
29581 - GTGCGCTCATGCTAGCTCCCATGCACTTATTACGATCCCTCTCGACGGATATACCTTC - 29640
- V R L M L A P M S L I T I P L D G Y T F
- C A S C * L P C H L L R S L S T D I P S
- A P H A S S H V T Y Y D P S R R I Y L L
29641 - TCGGGATTACACATTTTAATTAATATCAGGATAGGGGTACACTAAAATTATCGAAGA - 29700
- S G L H I L I K I I T I G V H * N Y R R
- R D Y T F * L K S S R * G Y T K I I E E
- G I T H F N * N H H D R G T L K L S K N

FIG. 5 Cont'd

29701 - ATCCTCTTACTGTTTTTTTTTTTTTTTTTTTTTTT - 29736
- I L L L F F F F F F F F F X
- S S Y C F F F F F F F F F X
- P L T V F F F F F F F F F X

FIG. 5 Cont'd

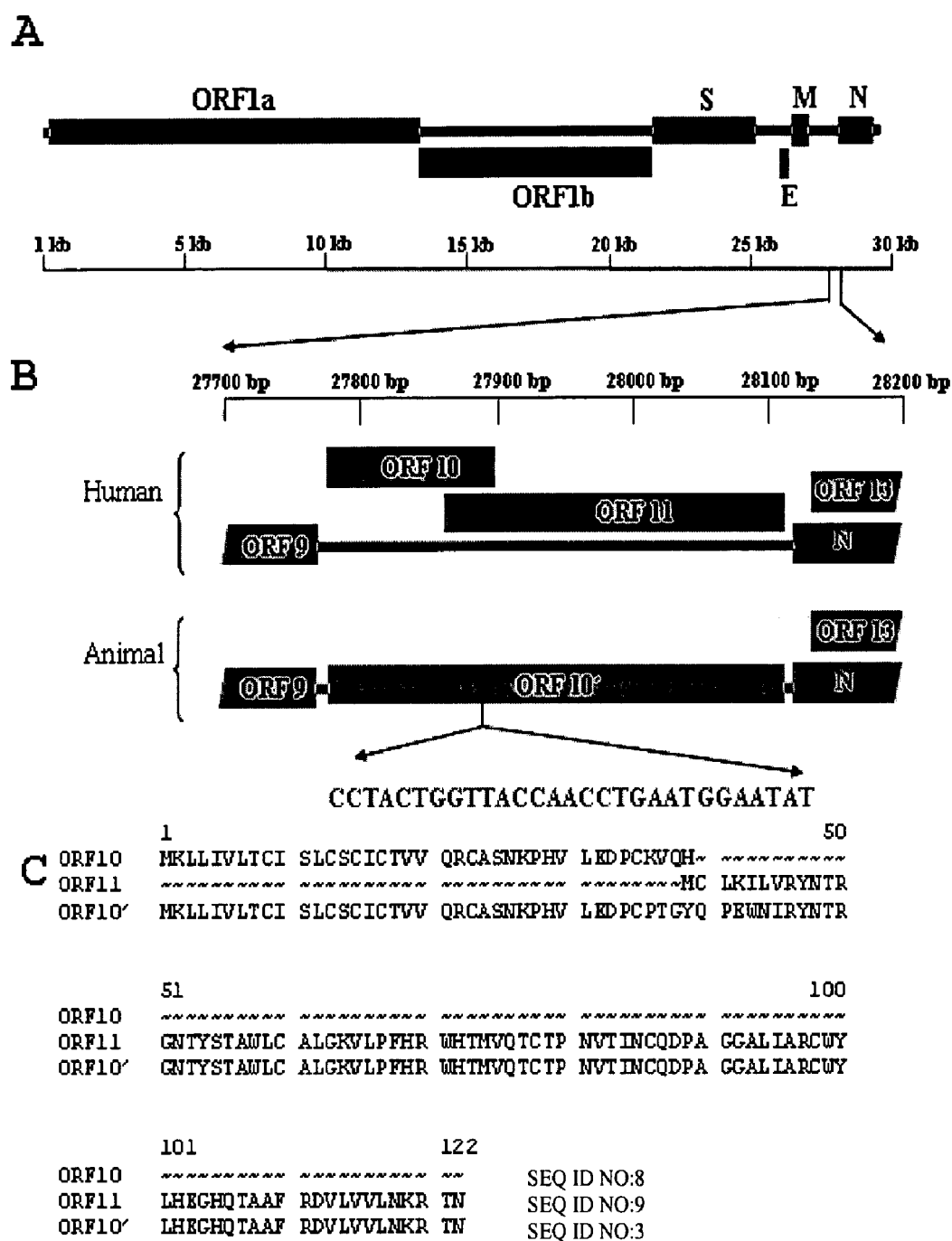
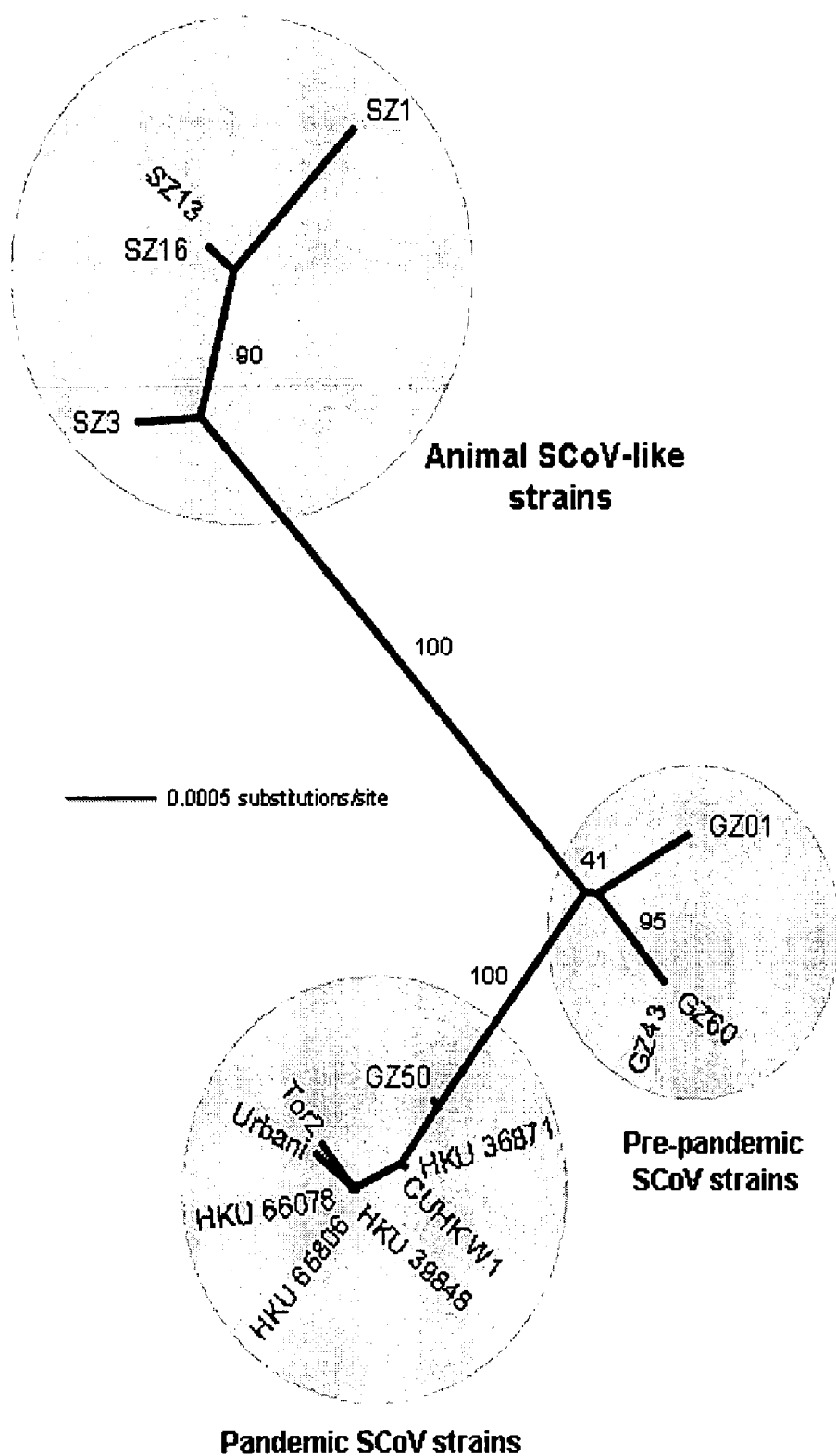


FIG. 6

1	ATG	AAA	CTT	CTC	ATT	GTT	TTG	ACT	TGT	ATT	TCT	CTA	TGC	AGT	TGC	45
1	M	K	L	L	I	V	L	T	C	I	S	L	C	S	C	15
46	ATA	CGC	ACT	GTA	GTA	CAG	CGC	TGT	GCA	TCT	AAT	AAA	CCT	CAT	GTG	90
16	I	R	T	V	V	Q	R	C	A	S	N	K	P	H	V	30
91	CTT	GAA	GAT	CCT	TGT	CCT	ACT	GGT	TAC	CAA	CCT	GAA	TGG	AAT	ATA	135
31	L	E	D	P	C	P	T	G	Y	Q	P	E	W	N	I	45
136	AGG	TAC	AAC	ACT	AGG	GGT	AAT	ACT	TAT	AGC	ACT	GCT	TGG	CTT	TGT	180
46	R	Y	N	T	R	G	N	T	Y	S	T	A	W	L	C	60
181	GCT	CTA	GGA	AAG	GTT	TTA	CCT	TTT	CAT	AGA	TGG	CAC	ACT	ATG	GTT	225
61	A	L	G	K	V	L	P	F	H	R	W	H	T	M	V	75
226	CAA	ACA	TGC	ACA	CCT	AAT	GTT	ACT	ATC	AAC	TGT	CAA	GAT	CCA	GCT	270
76	Q	T	C	T	P	N	V	T	I	N	C	Q	D	P	A	90
271	GGT	GGT	GCG	CTT	ATA	GCT	AGG	TGT	TGG	TAC	CTT	CAT	GAA	GGT	CAC	315
91	G	G	A	L	I	A	R	C	W	Y	L	H	E	G	H	105
316	CAA	ACT	GCT	GCA	TTT	AGA	GAC	GTA	CTT	GTT	GTT	TTA	ACT	AAA	CGA	360
106	Q	T	A	A	F	R	D	V	L	V	V	L	T	K	R	120
361	ACA	AAT	TAA													369
121	T	N	*													

FIG. 7

**FIG. 8**

ISOLATION AND CHARACTERIZATION OF THE PRECURSOR VIRUS OF HUMAN SARS VIRUS: SARS-ASSOCIATED CORONA VIRUS-LIKE VIRUS

This application claims priority benefit to U.S. provisional application No. 60/473,255 filed May 22, 2003, which is incorporated herein by reference in its entirety.

The instant application contains a lengthy Sequence Listing which is being concurrently submitted via triplicate CD-R in lieu of a printed paper copy, and is hereby incorporated by reference in its entirety. Said CD-R, recorded on May 24, 2004, are labeled "CRF", "Copy 1" and "Copy 2", respectively, and each contains only one identical 1.56 Mb file (V9661081.APP).

1. INTRODUCTION

The present invention relates to isolation and characterization of a class of isolated novel viruses which is the precursor of the virus causing Severe Acute Respiratory Syndrome (SARS) in humans ("hSARS virus"). The precursor virus which is a SARS coronavirus-like virus ("SCoV-like virus") is identified to be morphologically and phylogenetically similar to hSARS virus. The present invention relates to a nucleotide sequence comprising the genomic sequence of the SCoV-like virus. The invention further relates to nucleotide sequences comprising a portion of the genomic sequence of the SCoV-like virus. The invention also relates to the deduced amino acid sequences of the SCoV-like virus. The invention further relates to the nucleic acids and peptides encoded by and/or derived from these sequences and their use in diagnostic methods and therapeutic methods. The invention further encompasses chimeric or recombinant viruses encoded by said nucleotide sequences and antibodies directed against polypeptides encoded by the nucleotide sequences. Furthermore, the invention relates to vaccine preparations comprising the SCoV-like virus, including recombinant and chimeric forms of said virus.

2. BACKGROUND OF THE INVENTION

Recently, there has been an outbreak of a typical pneumonia in Guangdong province in mainland China. Between November 2002 and March 2003, there were 792 reported cases with 31 fatalities (WHO. Severe Acute Respiratory Syndrome (SARS) *Weekly Epidemiol Rec.* 2003; 78: 86). In response to this crisis, the Hospital Authority in Hong Kong has increased the surveillance on patients with severe atypical pneumonia. In the course of this investigation, a number of clusters of health care workers with the disease were identified. In addition, there were clusters of pneumonia incidents among persons in close contact with those infected. The disease was unusual in its severity and its progression in spite of the antibiotic treatment typical for the bacterial pathogens that are known to be commonly associated with atypical pneumonia. The disease was given the acronym Severe Acute Respiratory Syndrome ("SARS"). The virus was isolated from the patients suffering from SARS in the recent outbreak of severe atypical pneumonia in China. The isolated virus is an enveloped, single-stranded RNA virus of positive polarity which belongs to the order, Nidovirales, of the family, Coronaviridae. The hSARS virus was deposited with China Center for Type Culture Collection (CCTCC) on Apr. 2, 2003 and accorded an accession number, CCTCC-V200303, which is incorporated by reference in its entirety.

The etiologic agent responsible for this disease is a novel coronavirus known as hSARS virus. The viral genome sequence taken together with the epidemiological evidence suggest that the SARS associated coronavirus (SCoV) crossed the species barrier from animals to humans in the recent past.

3. SUMMARY OF INVENTION

The present invention is based upon the inventors' isolation and identification of a class of novel viruses which is the precursor of the virus causing Severe Acute Respiratory Syndrome in humans ("hSARS virus"). The precursor virus which is a SARS coronavirus-like virus ("SCoV-like virus") is identified to be morphologically and phylogenetically similar to hSARS virus.

An investigation was carried out in a retail live animal market in Guangdong, mainland China, the hypothetical birthplace of SARS, to better understand the animal reservoir of this virus. SCoV-like viruses were isolated from 4 of 6 Himalayan palm civets (*Paguma larvata*, Family Viverridae) and the serum from three of these animals neutralized the virus. Evidence of virus infection was also detected in a raccoon dog (*Nyctereutes procyonoides*) and Chinese ferret badger (*Melogale moschata*). Phylogenetic analysis indicates that these animal viruses have an ancestral relationship with the human SCoV with which they share genetic similarity. Sequence analysis revealed that all the animal virus isolates retain an "additional" 29 nucleotide sequence (SEQ ID NO:1) which is not found in most human virus isolates which results in the nucleotide sequence of SEQ ID NO:2 encoding a new putative protein of 122 amino acids (SEQ ID NO:3). The detection of SCoV-like viruses in small wild mammals found in live retail markets supplying the restaurant trade in Guangdong indicates how this virus may have crossed from its animal reservoir to humans. These findings are important for public health and may provide clues to understanding the inter-species transmission events relevant to the genesis of novel emerging diseases.

Accordingly, the present invention relates to a nucleotide sequence comprising the genomic sequence of the SCoV-like virus. The invention further relates to nucleotide sequences comprising a portion of the genomic sequence of the SCoV-like virus. The invention also relates to the deduced amino acid sequences of the SCoV-like virus. In specific embodiments, the invention provides a virus comprising a nucleic acid sequence of SEQ ID NO:1 or 2. In specific embodiments, the invention provides a virus comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence of SEQ ID NO:3. The invention further relates to the nucleic acids and peptides encoded by and/or derived from these sequences. In a specific embodiment, the invention provides the isolated SCoV-like virus that morphologically and phylogenetically relates to hSARS virus and comprises the nucleotide sequence of SEQ ID NO:1 in its genome. In a preferred embodiment, the virus comprises a nucleotide sequence of SEQ ID NO:1, a portion thereof, a complement thereof, or that hybridizes to the complement of SEQ ID NO:1. In another specific embodiment, the virus preferably further comprises a nucleotide sequence of SEQ ID NO: 2, a portion thereof, a complement thereof, or portions that hybridizes to the complement of SEQ ID NO:2, in its genome. In a specific embodiment, the present invention provides isolated nucleic acid molecules comprising or, alternatively, consisting of the nucleotide sequence of SEQ ID NO:1, a complement thereof or a portion thereof, preferably at least 3, 4, 5,

6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides of the nucleic acid sequence of SEQ ID NO:1. In another specific embodiment, the invention provides isolated nucleic acid molecules comprising or, alternatively, consisting of the nucleotide sequence of SEQ ID NO:2, a complement thereof, or portions thereof, preferably at least, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 320, 340, 360, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:2. In yet another specific embodiment, the present invention provides isolated nucleic acid molecules further comprising or, alternatively, consisting of the nucleotide sequence of SEQ ID NO:4, a complement thereof or a portion thereof, preferably at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000, 21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:4, or a complement thereof. Furthermore, in another specific embodiment, the invention provides isolated nucleic acid molecules comprising SEQ ID NO:1 and a sequence which hybridizes under stringent conditions, as defined herein, to a nucleic acid molecule having the sequence of SEQ ID NO:4, or a complement, or a portion thereof. In one embodiment, the invention provides an isolated nucleic acid molecule which is antisense to the coding strand of a nucleic acid of the invention. In another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, or 28 contiguous nucleotides of the nucleotide sequence of SEQ ID NO:1, or a complement thereof. In yet another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively consisting of nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 320, 340, 360, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:2, or a complement thereof. In yet another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000, 21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000 or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:4, or a complement thereof (SEQ ID NO:1102).

The invention further provides proteins or polypeptides that are isolated from the SCoV-like virus, including viral proteins isolated from cells infected with the virus but not present in comparable uninfected cells. In a specific embodiment, the polypeptide comprises the sequence of SEQ ID NO:3. The invention further provides proteins or polypeptides shown in FIG. 4 (SEQ ID NOS:12-233, 235-729 and 731-1101), 5 (SEQ ID NOS:12-233, 235-729 and 731-1101), and 7 (SEQ ID NO:3). The polypeptides or the proteins of the present invention preferably having a biological activity of the protein (including antigenicity and/or

immunogenicity) encoded by the sequence of SEQ ID NO:1, 2, a portion thereof, or their complements. In other embodiments, the polypeptides or the proteins of the present invention have a biological activity of the protein (including antigenicity and/or immunogenicity) encoded by a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000, 21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000 or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:4, or a complement thereof (SEQ ID NO:1102).

In one aspect, the invention provides a method for propagating the SCoV-like virus in host cells comprising infecting the host cells with the isolated SCoV-like virus, culturing the host cells to allow the virus to multiply, and harvesting the resulting virions. Also provided by the present invention are host cells that are infected with the SCoV-like virus. In specific embodiments, the host cells are from animals for example, but not limited to, feline, canine, palm civet, raccoon-dog, or ferret badger. In another aspect, the invention relates to the use of the isolated SCoV-like virus for diagnostic and therapeutic methods. In a specific embodiment, the invention provides a method of detecting in a biological sample an antibody immunospecific for the SCoV-like virus using the isolated SCoV-like virus or any proteins or polypeptides thereof. In another specific embodiment, the invention provides a method of screening for an antibody which immunospecifically binds and neutralizes SCoV-like viruses. Such an antibody is useful for a passive immunization or immunotherapy of a subject infected with a SCoV-like virus.

The invention further relates to the use of the sequence information of the isolated virus for diagnostic and therapeutic methods. In a specific embodiment, the invention provides nucleic acid molecules which are suitable for use as primers consisting of or comprising the nucleotide sequence of SEQ ID NO:1, 2, 4, or a complement thereof, or at least a portion of the nucleotide sequence thereof. In another specific embodiment, the invention provides nucleic acid molecules which are suitable for hybridization to SCoV-like viral nucleic acid, including, but not limited to, as PCR primers, Reverse Transcriptase primers, probes for Southern analysis or other nucleic acid hybridization analysis for the detection of SCoV-like nucleic acids, e.g., consisting of or comprising the nucleotide sequence of SEQ ID NO:1, 2, 4, or a complement thereof, or a portion thereof. The invention further encompasses chimeric or recombinant viruses encoded in whole or in part by said nucleotide sequences.

The invention further provides antibodies that specifically bind a polypeptide of the invention encoded by the nucleotide sequence of SEQ ID NO:1, 2, 4, or a fragment thereof, or encoded by a nucleic acid comprising a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO:1, 2, or 4, and/or any SCoV-like viral epitope, having one or more biological activities of a polypeptide of the invention. These polypeptides include those shown in FIG. 4 (SEQ ID NOS:12-233, 235-729 and 731-1101), 5 (SEQ ID NOS:1103-1583, 1585-1958 and 1960-2464), and 7 (SEQ ID NO:3). The invention further provides antibodies that specifically bind polypeptides of the invention encoded by a nucleic acid comprising a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO:1, 2, or 4, and/or any SCoV-like viral epitope, having one or more

biological activities of a polypeptide of the invention. Such antibodies include, but are not limited to polyclonal, monoclonal, bi-specific, multi-specific, human, humanized, chimeric antibodies, single chain antibodies, Fab fragments, F(ab')₂ fragments, disulfide-linked Fvs, intrabodies and fragments containing either a VL or VH domain or even a complementary determining region (CDR) that specifically binds to a polypeptide of the invention.

In one embodiment, the invention provides methods for detecting the presence, activity or expression of the SCoV-like virus of the invention in a biological material, such as cells, blood, sputum, stool, saliva, urine, and so forth. The increased or decreased activity or expression of the SCoV-like virus in a sample relative to a control sample can be determined by contacting the biological material with an agent which can detect directly or indirectly the presence, activity or expression of the SCoV-like virus. In a specific embodiment, the detecting agents are the antibodies or nucleic acid molecules of the present invention.

In another embodiment, the invention provides vaccine preparations, comprising the SCoV-like virus, including recombinant and chimeric forms of said virus, or protein subunits of the virus. In a specific embodiment, the vaccine preparations of the present invention comprise live but attenuated SCoV-like virus with or without adjuvants. In another specific embodiment, the vaccine preparations of the invention comprise an inactivated or killed SCoV-like virus. Such attenuated or inactivated viruses may be prepared by a series of passages of the virus through the host cells or by preparing recombinant or chimeric forms of virus. Accordingly, the present invention further provides methods of preparing recombinant or chimeric forms of SCoV-like virus. In another specific invention, the vaccine preparations of the present invention comprise a nucleic acid or fragment of the SCoV-like virus, e.g., the virus having nucleic acid molecules having the sequence of SEQ ID NO. 1, 2, 4, or a fragment thereof, or a complement thereof. In another embodiment, the invention provides vaccine preparations comprising one or more polypeptides isolated from or produced from nucleic acid of SCoV-like virus. In a specific embodiment, the vaccine preparations comprise a polypeptide of the invention encoded by the nucleotide sequence of SEQ ID NO:1, 2, 4, or a fragment thereof. In a specific embodiment, the vaccine preparations comprise polypeptides of the invention as shown in FIG. 4 (SEQ ID NOS: 12-233, 235-729 and 731-1101), 5 (SEQ ID NOS:1103-1583, 1585-1958 and 1960-2464), or 7 (SEQ ID NO:3).

In another aspect, the present invention provides pharmaceutical compositions comprising anti-viral agents of the present invention and a pharmaceutically acceptable carrier. In a specific embodiment, the anti-viral agent of the invention is an antibody that immunospecifically binds SCoV-like virus or any SCoV-like viral epitope. In another specific embodiment, the anti-viral agent is a polypeptide or protein of the present invention or nucleic acid molecule of the invention. The invention also provides kits containing a pharmaceutical composition of the present invention.

3.1 Definitions

The term "an antibody or an antibody fragment that immunospecifically binds a polypeptide of the invention" as used herein refers to an antibody or a fragment thereof that immunospecifically binds to the polypeptide encoded by the nucleotide sequence of the invention, or a fragment of thereof, and does not non-specifically bind to other polypeptides. An antibody or a fragment thereof that immunospe-

cifically binds to the polypeptide of the invention may cross-react with other antigens. Preferably, an antibody or a fragment thereof that immunospecifically binds to a polypeptide of the invention does not cross-react with other antigens. An antibody or a fragment thereof that immunospecifically binds to the polypeptide of the invention, can be identified by, for example, immunoassays or other techniques known to those skilled in the art.

An "isolated" or "purified" or "cloned" peptide or protein is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of a polypeptide/protein in which the polypeptide/protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, a polypeptide/protein that is substantially free of cellular material includes preparations of the polypeptide/protein having less than about 30%, 20%, 10%, 5%, 2.5%, or 1%, (by dry weight) of contaminating protein. When the polypeptide/protein is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, 10%, or 5% of the volume of the protein preparation. When polypeptide/protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, i.e., it is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. Accordingly, such preparations of the polypeptide/protein have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than polypeptide/protein fragment of interest. In a preferred embodiment of the present invention, polypeptides/proteins are isolated or purified.

An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid molecule. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. In a preferred embodiment of the invention, nucleic acid molecules encoding polypeptides/proteins of the invention are isolated or purified. The term "isolated" nucleic acid molecule does not include a nucleic acid that is a member of a library that has not been purified away from other library clones containing other nucleic acid molecules.

The term "portion" or "fragment" as used herein refers to a fragment of a nucleic acid molecule containing at least about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000, 21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000, or more contiguous nucleic acids in length of the relevant nucleic acid molecule and having at least one functional feature of the nucleic acid molecule (or the encoded protein has one functional feature of the protein encoded by the nucleic acid molecule); or a fragment of a protein or a polypeptide containing at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 320, 340, 360, 400,

500, 600, 700, 800, 900, 1,000, 1,500, 2,000, 2,500, 3,000, 3,500, 4,000, 4,100, 4,200, 4,300, 4,350, 4,360, 4,370, 4,380 amino acid residues in length of the relevant protein or polypeptide and having at least one functional feature of the protein or polypeptide.

The term "having a biological activity of the protein" or "having biological activities of the polypeptides of the invention" refers to the characteristics of the polypeptides or proteins having a common biological activity similar or identical structural domain and/or having sufficient amino acid identity to the polypeptide encoded by the nucleic acid of the present invention. Such common biological activities of the polypeptides of the invention include antigenicity and immunogenicity.

The term "under stringent condition" refers to hybridization and washing conditions under which nucleotide sequences having at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% identity to each other remain hybridized to each other. Such hybridization conditions are described in, for example but not limited to, Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6.; Basic Methods in Molecular Biology, Elsevier Science Publishing Co., Inc., N.Y. (1986), pp. 75-78, and 84-87; and Molecular Cloning, Cold Spring Harbor Laboratory, N.Y. (1982), pp. 387-389, and are well known to those skilled in the art. A preferred, non-limiting example of stringent hybridization conditions is hybridization in 6x sodium chloride/sodium citrate (SSC), 0.5% SDS at about 68° C. followed by one or more washes (e.g., about 5 to 30 min each) in 2xSSC, 0.5% SDS at room temperature. Another preferred, non-limiting example of stringent hybridization conditions is hybridization in 6xSSC at about 45° C. followed by one or more washes (e.g., about 5 to 30 min each) in 0.2xSSC, 0.1% SDS at about 50-65° C.

The term "variant" as used herein refers either to a naturally occurring genetic mutant of SCoV-like virus or a recombinantly prepared variation of SCoV-like virus each of which contain one or more mutations in its genome compared to the hSARS virus. The term "variant" may also refer either to a naturally occurring variation of a given peptide or a recombinantly prepared variation of a given peptide or protein in which one or more amino acid residues have been modified by amino acid substitution, addition, or deletion.

4. BRIEF DESCRIPTION OF FIGURES

FIGS. 1A and B show the characteristics of animal SARS-CoV-like virus grown in FRhK-4 cells. (A) shows a negatively stained (potassium phosphotungstate, 2%) preparations of an animal virus isolate showing particles with club-shaped spikes surrounding the periphery of the particles. (B) shows a thin-section electron microscope view of the viral particles growing inside a cell (FRhK-4) and released through cell membrane.

FIG. 2 shows the additional 29 nucleotides (SEQ ID NO:1) found in animal SCoV-like virus.

FIG. 3 shows the entire genomic DNA sequence (SEQ ID NO:4) of the SARS virus deposited in GenBank with accession number AY278554.

FIG. 4 shows the deduced amino acid sequences (SEQ ID NOS:12-233, 235-729 and 731-1101) obtained from SEQ ID NO:4 in three frames. An asterisk (*) indicates a stop codon which marks the end of a peptide.

FIG. 5 shows the deduced amino acid sequences obtained from the complement (SEQ ID NO:1102) of SEQ ID NO:4 in three frames. An asterisk (*) indicates a stop codon which marks the end of a peptide.

FIG. 6 shows the genomic organization of human and animal SCoV-like viruses. (A) Genetic organization of SCoV-like viruses found in humans and animals. ORFs 1a and 1b, encoding the nonstructural polyproteins, and those encoding the S, E, M, and N structural proteins are indicated. (B) Expanded view of the SCoV genomic sequence (27700 nt to 28200 nt, based on AY278554 numbering). ORFs for putative proteins (9-11 and 13) and for N in human isolates are indicated (Peiris et al., 2003, *Lancet* 361:1319; Zhong et al., 2003, *Lancet* 362:1353). An extra 29 nucleotide sequence is present down-stream of the nucleotide of 27868 (based on AY278554 numbering) of the animal SCoV. The presence of this 29 nt sequence in animal isolates results in fusing the ORFs 10 (SEQ ID NO:8) and 11 (SEQ ID NO:9) (upper panel) into a new ORF (lower panel; ORF10'; SEQ ID NO:3). (C) Protein sequence alignment of ORF10 and 11 from human isolates and ORF 10' from animal isolates (SCoV-like virus strain SZ3, AY304486).

FIG. 7 shows the nucleotide sequence (SEQ ID NO:2) and its deduced amino acid sequence (SEQ ID NO:3) of a portion of the genome of SCoV-like virus (strain SZ3, AY304486) comprising SEQ ID NO:1, which is the additional 29 nucleotide residues not found in hSARS virus, resulting in encoding a new putative protein of 122 amino acids (SEQ ID NO:3).

FIG. 8 shows a phylogenetic analysis of a partial nucleotide acid sequence of spike gene of SCoV-like viruses. An unrooted phylogram derived from the partial nucleotide sequence of representative SCoV S genes (S coding region residue 344 to 3765, 3422 bp). Multiple sequence alignments were done using Clustal X 1.81 and trees generated using Neighbor-Joining algorithms within PAUP 4.0b10. Bootstrap scores are percentages out of 1000 replicates. Similar tree topologies were seen with Maximum Parsimony analysis (data not shown). Except for the viruses sequenced in current study, the other sequences used in the analysis could be found in GenBank with accession number: AY278741, AY278554, AY278491, AY274119, and AY278489, all of which are incorporated by reference in their entirety.

5. DETAILED DESCRIPTION OF THE INVENTION

Severe acute respiratory syndrome (SARS) is a recently emerged human disease associated with pneumonia. This disease was first recognized in Guangdong Province, China in November 2002. Subsequent to its introduction to Hong Kong in mid February 2003, the virus spread to more than 28 countries causing disease in over 7,900 patients across 5 continents. The disease is unusual in its predilection to affect health care workers. A novel coronavirus (SCoV) was identified as the etiological agent of SARS (Peiris et al., 2003, *Lancet* 361:1319; Ksiazek et al., 2003, *N. Engl. J. Med.* 348:1953) and the virus causes a similar disease in cynomolgous macaques. Fouchier et al., 2003, *Nature* 423:240. While the majority of patients with SARS seroconvert to SCoV, patients with other respiratory disease and healthy blood donors had no detectable antibody. Peiris et al., 2003, *Lancet* 361:1319; Zhong et al., 2003, *Lancet* 362:1353). These results suggest that the human SCoV is an animal virus that crossed to humans relatively recently. Thus, identifying the animal reservoir is of major scientific interest as

well as public health importance. A range of domestic and wild mammals in Guangdong Province were examined.

The present invention is based upon the inventor's isolation and identification of a class of novel viruses which is the precursor of the virus causing Severe Acute Respiratory Syndrome in humans ("hSARS virus"). The precursor virus which is a SARS coronavirus-like virus ("SCoV-like virus") is identified to be morphologically and phylogenetically similar to hSARS virus.

An investigation was carried out in a retail live animal market in Guangdong, mainland China, the hypothetical birthplace of SARS, to better understand the animal reservoir of this virus. SCoV-like coronaviruses were isolated from 4 of 6 Himalayan palm civets (*Paguma larvata*, Family Viverridae) and the serum from one of these animals neutralized the virus. Phylogenetic analysis indicates that these animal viruses have an ancestral relationship with the human SCoV with which they share genetic similarity. Sequence analysis revealed that all the animal virus isolates retain an "additional" 29 nucleotide residues which are not found in most human virus isolates which results in encoding a new putative protein of 122 amino acids. These 29 nucleotide residues are inserted at the nucleotide position corresponding to 27859 of GenBank accession no: AY278554 or 27874 of AY274119. The detection of SCoV-like viruses in small wild mammals found in live retail markets supplying the restaurant trade in Guangdong indicates how this virus may have crossed from its animal reservoir to humans. These findings are important for public health and may provide clues to understanding the inter-species transmission events relevant to the genesis of novel emerging diseases.

Accordingly, the present invention relates to a nucleotide sequence comprising the genomic sequence of the SCoV-like virus. The invention further relates to nucleotide sequences comprising a portion of the genomic sequence of the SCoV-like virus. The invention also relates to the deduced amino acid sequences of the SCoV-like virus. The invention further relates to the nucleic acids and peptides encoded by and/or derived from these sequences. In a specific embodiment, the invention provides the isolated SCoV-like virus that morphologically and phylogenetically relates to hSARS virus and comprises the nucleotide sequence of SEQ ID NO:1 in its genome. In another embodiment, the virus comprises a nucleotide sequence of SEQ ID NO:2. In another embodiment, the virus comprises a nucleotide sequence that encodes an amino acid sequence of SEQ ID NO:3. In a preferred embodiment, the virus comprises a nucleotide sequence of SEQ ID NO:1. In another specific embodiment, the virus preferably further comprises a nucleotide sequence of SEQ ID NO:2, portions thereof, or portions that hybridizes to the complement of SEQ ID NO:2, in its genome. In a specific embodiment, the present invention provides isolated nucleic acid molecules comprising or, alternatively, consisting of the nucleotide sequence of SEQ ID NO:1, a complement thereof or a portion thereof, preferably at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides of the nucleic acid sequence of SEQ ID NO:1. In another specific embodiment, the present invention provides isolated nucleic acid molecules comprising or, alternatively, consisting of the nucleotide sequence of SEQ ID NO:2, a complement thereof or a portion thereof, preferably at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 320, 340, 360, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:2, or a complement thereof. In yet another specific embodiment, the present

invention provides isolated nucleic acid molecules further comprising or, alternatively, consisting of the nucleotide sequence of SEQ ID NO:4, a complement thereof or a portion thereof, preferably at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000, 21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:4, or a complement thereof. Furthermore, in another specific embodiment, the invention provides isolated nucleic acid molecules which hybridize under stringent conditions, as defined herein, to a nucleic acid molecule having the sequence of SEQ ID NO:1, 2, 4, or a complement, or a portion thereof. In one embodiment, the invention provides an isolated nucleic acid molecule which is antisense to the coding strand of a nucleic acid of the invention. In another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively, consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, or 28 contiguous nucleotides of the nucleotide sequence of SEQ ID NO:1, or a complement thereof. In another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively, consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 320, 340, 360, or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:2, or a complement thereof. In yet another specific embodiment, the invention provides isolated polypeptides or proteins that are encoded by a nucleic acid molecule comprising or, alternatively, consisting of a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000, 21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000 or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:4, or a complement thereof.

The invention further provides proteins or polypeptides that are isolated from the SCoV-like virus, including viral proteins isolated from cells infected with the virus but not present in comparable uninfected cells. Specifically, the protein comprises the amino acid sequence of SEQ ID NO:3 or encoded by the nucleic acid of SEQ ID NO:2. The invention further provides proteins or polypeptides shown in FIG. 4 (SEQ ID NOS:12-233, 235-729 and 731-1101) and 5 (SEQ ID NOS:1103-1583, 1585-1958 and 1960-2464). The polypeptides or the proteins of the present invention preferably have a biological activity of the protein (including antigenicity and/or immunogenicity) encoded by the sequence of SEQ ID NO:1, 2, or a portion thereof, or their complements. In other embodiments, the polypeptides or the proteins of the present invention have a biological activity of the protein (including antigenicity and/or immunogenicity) encoded by a nucleotide sequence that is at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 100, 150, 200, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1,000, 1,050, 1,100, 1,150, 1,200, 2,000, 3,000, 4,000, 5,000, 6,000, 7,000, 8,000, 9,000, 10,000, 11,000, 12,000, 13,000, 14,000, 15,000, 16,000, 17,000, 18,000, 19,000, 20,000,

21,000, 22,000, 23,000, 24,000, 25,000, 26,000, 27,000, 28,000, 29,000 or more contiguous nucleotides of the nucleotide sequence of SEQ ID NO:4, or a complement thereof.

In one aspect, the invention provides a method for propagating the SCoV-like virus in host cells comprising infecting the host cells with the isolated SCoV-like virus, culturing the host cells to allow the virus to multiply, and harvesting the resulting virions. Also provided by the present invention are host cells that are infected with the SCoV-like virus. In another aspect, the invention relates to the use of the isolated SCoV-like virus for diagnostic and therapeutic methods. In a specific embodiment, the invention provides a method of detecting in a biological sample an antibody immunospecific for the SCoV-like virus using the isolated SCoV-like virus or any proteins or polypeptides thereof. In another specific embodiment, the invention provides a method of screening for an antibody which immunospecifically binds and neutralizes SCoV-like virus. Such an antibody is useful for a passive immunization or immunotherapy of a subject infected with SCoV-like virus.

The invention further relates to the use of the sequence information of the isolated virus for diagnostic and therapeutic methods. In a specific embodiment, the invention provides nucleic acid molecules which are suitable for use as primers consisting of or comprising the nucleotide sequence of SEQ ID NO:1, 2, 4, or a complement thereof, or at least a portion of the nucleotide sequence thereof. In another specific embodiment, the invention provides nucleic acid molecules which are suitable for hybridization to SCoV-like nucleic acid, including, but not limited to, as PCR primers, Reverse Transcriptase primers, probes for Southern analysis or other nucleic acid hybridization analysis for the detection of SCoV-like nucleic acids, e.g., consisting of or comprising the nucleotide sequence of SEQ ID NO:1, 2, 4, or a complement thereof, or a portion thereof. The invention further encompasses chimeric or recombinant viruses encoded in whole or in part by said nucleotide sequences.

The invention further provides antibodies that specifically bind a polypeptide of the invention encoded by the nucleotide sequence of SEQ ID NO:1, 2, or 4, or a fragment thereof, or encoded by a nucleic acid comprising a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO:1, 2, or 4, and/or any SCoV-like viral epitope, having one or more biological activities of a polypeptide of the invention. The invention further provides antibodies that specifically bind polypeptides of the invention encoded by the nucleotide sequence of SEQ ID NO:1, 2, or 4, or a fragment thereof. These polypeptides include those shown in FIGS. 4, 5 and 7. The invention further provides antibodies that specifically bind polypeptides of the invention encoded by a nucleic acid comprising a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO:1, 2, 4, and/or any SCoV viral epitope, having one or more biological activities of a polypeptide of the invention. Such antibodies include, but are not limited to polyclonal, monoclonal, bi-specific, multi-specific, human, humanized, chimeric antibodies, single chain antibodies, Fab fragments, F(ab')₂ fragments, disulfide-linked Fvs, intrabodies and fragments containing either a VL or VH domain or even a complementary determining region (CDR) that specifically binds to a polypeptide of the invention.

In one embodiment, the invention provides methods for detecting the presence, activity or expression of the SCoV-like virus of the invention in a biological material, such as cells, blood, sputum, stool, saliva, urine, and so forth. The increased or decreased activity or expression of the SCoV-

like virus in a sample relative to a control sample can be determined by contacting the biological material with an agent which can detect directly or indirectly the presence, activity or expression of the SCoV-like virus. In a specific embodiment, the detecting agents are the antibodies or nucleic acid molecules of the present invention.

In another embodiment, the invention provides vaccine preparations, comprising the SCoV-like virus, including recombinant and chimeric forms of said virus, or protein subunits of the virus. In a specific embodiment, the vaccine preparations of the present invention comprise live but attenuated SCoV-like virus with or without adjuvants. In another specific embodiment, the vaccine preparations of the invention comprise an inactivated or killed SCoV-like virus. Such attenuated or inactivated viruses may be prepared by a series of passages of the virus through the host cells or by preparing recombinant or chimeric forms of virus. Accordingly, the present invention further provides methods of preparing recombinant or chimeric forms of SCoV-like virus. In another specific invention, the vaccine preparations of the present invention comprise a nucleic acid or fragment of the SCoV-like virus, e.g., the virus having nucleic acid molecules having the sequence of SEQ ID NO. 1, 2, 4, or a fragment thereof. In another embodiment, the invention provides vaccine preparations comprising one or more polypeptides isolated from or produced from nucleic acid of SCoV-like virus. In a specific embodiment, the vaccine preparations comprise a polypeptide of the invention encoded by the nucleotide sequence of SEQ ID NO:1, 2, 4, or a fragment thereof. In a specific embodiment, the vaccine preparations comprise polypeptides of the invention as shown in FIG. 4, 5, or 7.

In another aspect, the present invention provides pharmaceutical compositions comprising anti-viral agents of the present invention and a pharmaceutically acceptable carrier. In a specific embodiment, the anti-viral agent of the invention is an antibody that immunospecifically binds SCoV-like virus or any SCoV-like viral epitope. In another specific embodiment, the anti-viral agent is a polypeptide or protein of the present invention or nucleic acid molecule of the invention. The invention also provides kits containing a pharmaceutical composition of the present invention.

Since the early cases of SARS in Guangdong reportedly occurred in restaurant workers handling wild mammals as exotic food (Zhong et al., 2003, *Lancet* 362:1353). A live animal retail market in Shenzhen was investigated. Animals were held, one per cage, in small wire cages. The animals sampled included seven wild, and one domestic animal species (Table 1). They originated from different regions of southern China and had been kept in separate storehouses before arrival to the market. The animals remain in the markets for a variable period of time and each stall holder has only a few animals of a given species. Animals from a different stalls within the market were sampled. Nasal and fecal swabs were collected and stored in viral transport medium. Where possible, blood samples were collected for serology. Prior to sampling, all animals were examined by a veterinary surgeon and confirmed to be free of overt disease.

Nasal and fecal swabs were obtained from 25 animals and tested for SCoV viral nucleic acid using RT-PCR for the N gene of the hSARS. Swabs from 4 of 6 Himalayan palm civets were positive in the RT-PCR assay (Table 1). All specimens were inoculated on to FRhk-4 cells as previously described for virus isolation (Peiris et al., 2003, *Lancet* 361:1319). Cytopathic effect was observed in infected cells after 2-3 days post-infection specimens from 4 Himalayan palm civets (*Paguma larvata*), two of whom were also

RT-PCR positive. Thus there was either RT-PCR or culture evidence of a virus in all 6 civets tested (Table 1). A virus was also detected by virus isolation and direct RT-PCR from the fecal swab of a Raccoon-dog (*Nyctereutes procyonoides*). No virus was detectable in 6 other species sampled. Electron microscopy of one infected cell supernatant (SZ16N) showed viral particles with a morphology comparable to a coronavirus (FIG. 1) and all the virus isolates were confirmed to be SCoV-like viruses by RT-PCR and direct sequencing of the PCR product. Sera from three animals had neutralizing antibody to the animal coronavirus; these were from a palm civet, Raccoon-dog and a Chinese ferret badger, respectively.

TABLE 1

Animal types tested and coronavirus detection						
Animal		Virus detection				Neutralizing
Sample	type	RT-PCR detection		Isolation		antibody titer
number	(Species)	Nasal	Fecal	Nasal	Fecal	to SZ16
SZ1	HPC	+	+			<20
SZ2	HPC	+	+			<20
SZ3	HPC	+	+	+		<20
SZ4	HB					<20
SZ5	B					<20
SZ6	DC					<20
SZ7	DC					<20
SZ8	CH					<20
SZ9	CH					<20
SZ10	CM					<20
SZ11	CFB					160
SZ12	CFB					<20
SZ13	RD		+		+	≥ 640
SZ14	CM					<20
SZ15	B					<20
SZ16	HPC	+	+	+	+	<20
SZ17	HPC			+		≥ 640
SZ18	B					<20
SZ19	CH					<20
SZ20	CH					<20
SZ21	DC					<20
SZ22	DC					<20
SZ23	HB					<20
SZ24	HB					<20
SZ25	HPC			+		<20

Abbreviation of animal species: HPC, Himalayan palm civet (*Paguma larvata*); HB, Hog-badger (*Arctonyx col-laris*); RD, Raccoon-dog (*Nyctereutes procyonoides*); B, Beaver (*Castor fiber*); CM, Chinese muntjac (*Muntiacus reevesi*); DC, Domestic cat (*Felis catus*); CH, Chinese Hare (*Lepus sinensis*); CFB, Chinese Ferret-Badger (*Melogale moschata*) [China species information system provided at the web site of Wildlife Conservation Society (WCS) and Institute of Zoology].

+ positive by RT-PCR or virus isolation, * the PCR product or virus isolates being sequenced.

Two of the virus isolates (SZ3N and SZ16N) isolated from the nasal swabs of palm civets were completely sequenced and the amino acid sequence deduced. Two other viruses were partially sequenced, from the S gene onward to the 3' end of the virus. The full-length genome sequences had 99.8% homology to the human SCoV indicating the human and animal SCoV-like viruses were closely related. Phylogenetic analysis of the S gene of both human and animal SCoV-like viruses indicated that the animal viruses are separate from the human virus cluster (FIG. 8). However, the viruses SZ1, SZ3 and SZ16 from palm civets were not clonally related (FIG. 8). The viruses SZ3 and SZ16 had 18 nucleotide differences between them over the 29,709 base pair genome while the human SCoV cluster of 5 geographically separated human viruses (GZ50, CUHK-W1, Tor-2, HKU-39848 and Urbani, FIG. 7) differed by only 14 nucleotides. On the other hand, animal viruses SZ13 (Raccoon-dog) and SZ16 (palm civet) were genetically almost identical.

When viruses in the human and animal groups are compared, 72 to 86 nucleotide differences were observed over the whole virus genome, many of them scattered across the whole genome. However, there were 19 consistent nucleotide differences between animal and human viruses localized in the S (Table 2) and M genes, 15 of them being non-synonymous mutations. Interestingly, some of the human virus isolates (e.g. GZ43 and GZ60) share some of the amino acid residues (positions 22192, 23470 and 23808, based on AY278554 numbering) with animal viruses (Table 2) suggesting that the human viruses isolated during the early phase of the SARS outbreak retained some of the "signatures" of the animal precursor.

TABLE 2

Nucleotide and amino acid substitutions of the SCoV-like viruses and SCoV								
Gene	S							
	Site*	22157	22192	22258	22555	22913	23148	23295
SZ3		A (K)	T (L)	A (K)	C (S)	A (K)	T (F)	C (P)
SZ16		A (K)	T (L)	A (K)	C (S)	A (K)	A (I)	C (P)
SZ1		A (K)	T (L)	A (K)	C (S)	A (K)	A (I)	C (P)
SZ13		A (K)	T (L)	A (K)	C (S)	A (K)	A (I)	C (P)
GZ43		C (N)	T (L)	C (T)	T (F)	T (N)	T (F)	T (S)
GZ60		C (N)	T (L)	C (T)	T (F)	T (N)	T (F)	T (S)
GZ50		C (N)	C (S)	C (T)	T (F)	T (N)	T (F)	T (S)
CUHK-W1		C (N)	C (S)	C (T)	T (F)	T (N)	T (F)	T (S)
HKU-36871		C (N)	C (S)	C (T)	T (F)	T (N)	T (F)	T (S)
HKU-39848		C (N)	C (S)	C (T)	T (F)	T (N)	T (F)	T (S)
HKU-66078		C (N)	C (S)	C (T)	T (F)	T (N)	T (F)	T (S)
HKU-65806		C (N)	C (S)	C (T)	T (F)	T (N)	T (F)	T (S)
Urbani		C (N)	C (S)	C (T)	T (F)	T (N)	T (F)	T (S)
Tor2		C (N)	C (S)	C (T)	T (F)	T (N)	T (F)	T (S)

TABLE 2-continued

Nucleotide and amino acid substitutions of the SCoV-like viruses and SCoV							
Gene	S						M
Site*	23578	23703	23737	23808	24156	24963	26395
SZ3	T (L)	G (A)	T (V)	G (D)	G (A)	G (E)	A (S)
SZ16	T (L)	G (A)	T (V)	G (D)	G (A)	G (E)	A (S)
SZ1	T (L)	G (A)	T (V)	G (D)	G (A)	G (E)	A (S)
SZ13	T (L)	G (A)	T (V)	G (D)	G (A)	G (E)	A (S)
GZ43	C (S)	A (T)	C (A)	G (D)	A (T)	A (K)	G (G)
GZ60	C (S)	A (T)	C (A)	G (D)	A (T)	A (K)	G (G)
GZ50	C (S)	A (T)	C (A)	G (D)	A (T)	A (K)	G (G)
CUHK-W1	C (S)	A (T)	C (A)	T (Y)	A (T)	A (K)	G (G)
HKU-36871	C (S)	A (T)	C (A)	T (Y)	A (T)	A (K)	G (G)
HKU-39848	C (S)	A (T)	C (A)	T (Y)	A (T)	A (K)	G (G)
HKU-66078	C (S)	A (T)	C (A)	T (Y)	A (T)	A (K)	G (G)
HKU-65806	C (S)	A (T)	C (A)	T (Y)	A (T)	A (K)	G (G)
Urbani	C (S)	A (T)	C (A)	T (Y)	A (T)	A (K)	G (G)
Tor2	C (S)	A (T)	C (A)	T (Y)	A (T)	A (K)	G (G)

Numbering based on AY278554.

The most striking genetic difference between the animal and human virus groups was that the human viruses (with the exception of GZ01) all share a 29 nucleotide acid (nt) deletion [5'-CCTACTGGTTACCAACCTGAATG-GAATAT-3' (SEQ ID NO:1), residue 27869 to 27897] at 246 nucleotide upstream of the start codon of the N gene. Sequence analysis of the animal isolates revealed that all of them retain this "additional" 29 nucleotide sequence. This 29 base pair deletion might have occurred during adaptation to humans and for to human to human transmission. Interestingly, the existence of this additional sequence in the animal viruses results in demolishing the open reading frames (ORFs) 10 and 11 (Marra et al., *Science* May 1 2003:1085953, electronically published at the web site of American Association for the Advancement of Science) and merging these two ORFs into a new ORF encoding a putative protein of 122 amino acid. This 122 amino acids putative peptide has a high homology to the putative proteins encoded by ORF10 and ORF12. Since the ORF11 does not have a typical transcription regulatory sequence for SCoV the putative ORF11 may be the direct result of the deletion of the 29 nt sequence. The loss of this peptide may help the virus in its adaptation to transmit efficiently from human to human.

Phylogenetic analysis of the S gene of both human and animal viruses indicated that the animal viruses are separated from the human virus cluster (FIG. 8). Taken together with the fact that most human SCoV have a deletion in the non-coding region of the genome, it is highly unlikely that the isolation of SCoV-like viruses in these wild animals is due to the reverse transmission of SCoV from human to animal. A more plausible hypothesis for these observations is that these animal viruses are the precursor of the human SCoV or that both the human and these animal viruses have been infected from the same source.

Of the eight animal species investigated in the market, two species, viz. palm civet and Raccoon-dog had virus isolated from them and a third, (Chinese ferret badger) had serological evidence of infection. It is clear that a number of these species can amplify the virus within the retail market setting and are probably important from the point of view of public health. These animals may be the natural reservoir infection in the wild or that both humans and civets, Raccoon-dog and ferret badgers were all infected from another animal source, which is in fact the true reservoir in nature. Alter-

natively, these market animals may be an intermediate host that, because of the culinary practices of southern China, brings the virus into close proximity with humans. However, the virus infected civets and Raccoon-dogs were apparently healthy suggesting that virus is well adapted to this species and may be in ecological equilibrium with each other. This shows that the civet (or Raccoon-dog) being a natural reservoir rather than a short-term incidental host.

5.1 Recombinant and Chimeric SCoV-Like Viruses

The present invention encompasses recombinant or chimeric viruses encoded by viral vectors derived from the genome of SCoV-like virus or natural variants thereof. In another specific embodiment, a recombinant virus is one derived from a natural variant of SCoV-like virus. A natural variant of SCoV-like virus has a sequence that is different from the genomic sequence (SEQ ID NO:4) of the hSARS virus, due to one or more naturally occurred mutations, including, but not limited to, point mutations, rearrangements, insertions, deletions etc., to the genomic sequence that may or may not result in a phenotypic change. In accordance with the present invention, a viral vector which is derived from the genome of the SCoV-like virus, is one that contains a nucleic acid sequence that encodes at least a part of one ORF of the virus. In a specific embodiment, the ORF comprises or consists of a nucleotide sequence of SEQ ID NO:1, 2, or 4, or a fragment thereof. In a specific embodiment, there are more than one ORF within the nucleotide sequence of SCoV-like virus, as shown in FIG. 4, 5 or 7, or a fragment thereof. In another embodiment, the polypeptide encoded by the ORF comprises or consists of an amino acid sequence of SEQ ID NO:3, or a fragment thereof, or shown in FIG. 4, 5, or 7, or a fragment thereof. In accordance with the present invention these viral vectors may or may not include nucleic acids that are non-native to the viral genome.

In another specific embodiment, a chimeric virus of the invention is a recombinant SCoV-like virus which further comprises a heterologous nucleotide sequence. In accordance with the invention, a chimeric virus may be encoded by a nucleotide sequence in which heterologous nucleotide sequences have been added to the genome or in which endogenous or native nucleotide sequences have been replaced with heterologous nucleotide sequences.

According to the present invention, the chimeric viruses are encoded by the viral vectors of the invention which further comprise a heterologous nucleotide sequence. In accordance with the present invention a chimeric virus is encoded by a viral vector that may or may not include nucleic acids that are non-native to the viral genome. In accordance with the invention a chimeric virus is encoded by a viral vector to which heterologous nucleotide sequences have been added, inserted or substituted for native or non-native sequences. In accordance with the present invention, the chimeric virus may be encoded by nucleotide sequences derived from different strains or variants of SCoV-like virus. In particular, the chimeric virus is encoded by nucleotide sequences that encode antigenic polypeptides derived from different strains or variants of SCoV-like virus.

A chimeric virus may be of particular use for the generation of recombinant vaccines protecting against two or more viruses (Tao et al., *J. Virol.* 72, 2955-2961; Durbin et al., 2000, *J. Virol.* 74, 6821-6831; Skiadopoulos et al., 1998, *J. Virol.* 72, 1762-1768 (1998); Teng et al., 2000, *J. Virol.* 74, 9317-9321). For example, it can be envisaged that a virus vector derived from the SCoV-like virus expressing one or more proteins of variants of SCoV-like virus, or vice versa, will protect a subject vaccinated with such vector against infections by both the native SCoV-like virus and the variant. Attenuated and replication-defective viruses may be of use for vaccination purposes with live vaccines as has been suggested for other viruses. (See, PCT WO 02/057302, at pp. 6 and 23, incorporated by reference herein).

In accordance with the present invention the heterologous sequence to be incorporated into the viral vectors encoding the recombinant or chimeric viruses of the invention include sequences obtained or derived from different strains or variants of SCoV-like virus.

In certain embodiments, the chimeric or recombinant viruses of the invention are encoded by viral vectors derived from viral genomes wherein one or more sequences, intergenic regions, termini sequences, or portions or entire ORF have been substituted with a heterologous or non-native sequence. In certain embodiments of the invention, the chimeric viruses of the invention are encoded by viral vectors derived from viral genomes wherein one or more heterologous sequences have been inserted or added to the vector.

The selection of the viral vector may depend on the species of the subject that is to be treated or protected from a viral infection. If the subject is human, then an attenuated SCoV-like virus can be used to provide the antigenic sequences.

In accordance with the present invention, the viral vectors can be engineered to provide antigenic sequences which confer protection against infection by the SCoV-like virus and natural variants thereof. The viral vectors may be engineered to provide one, two, three or more antigenic sequences. In accordance with the present invention the antigenic sequences may be derived from the same virus, from different strains or variants of the same type of virus, or from different viruses.

The expression products and/or recombinant or chimeric virions obtained in accordance with the invention may advantageously be utilized in vaccine formulations. The expression products and chimeric virions of the present invention may be engineered to create vaccines against a broad range of pathogens, including viral and bacterial antigens, tumor antigens, allergen antigens, and auto antigens involved in autoimmune disorders. In particular, the chimeric virions of the present invention may be engineered

to create vaccines for the protection of a subject from infections with SCoV-like virus and variants thereof.

In certain embodiments, the expression products and recombinant or chimeric virions of the present invention may be engineered to create vaccines against a broad range of pathogens, including viral antigens, tumor antigens and autoantigens involved in autoimmune disorders. One way to achieve this goal involves modifying existing SCoV-like viral genes to contain foreign sequences in their respective external domains. Where the heterologous sequences are epitopes or antigens of pathogens, these chimeric viruses may be used to induce a protective immune response against the disease agent from which these determinants are derived.

Thus, the present invention relates to the use of viral vectors and recombinant or chimeric viruses to formulate vaccines against a broad range of viruses and/or antigens. The present invention also encompasses recombinant viruses comprising a viral vector derived from the SCoV-like virus or variants thereof which contains sequences which result in a virus having a phenotype more suitable for use in vaccine formulations, e.g., attenuated phenotype or enhanced antigenicity. The mutations and modifications can be in coding regions, in intergenic regions and in the leader and trailer sequences of the virus.

The invention provides a host cell comprising a nucleic acid or a vector according to the invention. Plasmid or viral vectors containing the polymerase components of SCoV-like virus are generated in prokaryotic cells for the expression of the components in relevant cell types (bacteria, insect cells, eukaryotic cells). Plasmid or viral vectors containing full-length or partial copies of the SCoV-like viral genome will be generated in prokaryotic cells for the expression of viral nucleic acids in-vitro or in-vivo. The latter vectors may contain other viral sequences for the generation of chimeric viruses or chimeric virus proteins, may lack parts of the viral genome for the generation of replication defective virus, and may contain mutations, deletions or insertions for the generation of attenuated viruses. In addition, the present invention provides a host cell infected with SCoV-like virus.

Infectious copies of SCoV-like virus (being wild type, attenuated, replication-defective or chimeric) can be produced upon co-expression of the polymerase components according to the state-of-the-art technologies described above.

In addition, eukaryotic cells, transiently or stably expressing one or more full-length or partial proteins can be used. Such cells can be made by transfection (proteins or nucleic acid vectors), infection (viral vectors) or transduction (viral vectors) and may be useful for complementation of mentioned wild type, attenuated, replication-defective or chimeric viruses.

The viral vectors and chimeric viruses of the present invention may be used to modulate a subject's immune system by stimulating a humoral immune response, a cellular immune response or by stimulating tolerance to an antigen. As used herein, a subject means: humans, primates, horses, cows, sheep, pigs, goats, dogs, cats, avian species, rodents, raccoon-dog, civet, and ferret.

5.2 Formulation of Vaccines and Antivirals

In a preferred embodiment, the invention provides a proteinaceous molecule or SCoV-like virus specific viral protein or functional fragment thereof encoded by a nucleic acid according to the invention. Useful proteinaceous molecules are for example derived from any of the genes or genomic fragments derivable from the virus according to the

invention, including envelop protein (E protein), integral membrane protein (M protein), spike protein (S protein), nucleocapsid protein (N protein), hemagglutinin esterase (HE protein), and RNA-dependent RNA polymerase. Such molecules, or antigenic fragments thereof, as provided herein, are for example useful in diagnostic methods or kits and in pharmaceutical compositions such as subunit vaccines. Particularly useful are polypeptides encoded by the nucleotide sequence of SEQ ID NO:1, 2, or 4, or as shown in FIGS. 4, 5, 7, or antigenic fragments thereof for inclusion as antigen or subunit immunogen, but inactivated whole virus can also be used. Particularly useful are also those proteinaceous substances that are encoded by recombinant nucleic acid fragments of the SCoV-like viral genome, of course preferred are those that are within the preferred bounds and metes of ORFs, in particular, for eliciting SCoV-like virus specific antibody or T cell responses, whether in vivo (e.g. for protective or therapeutic purposes or for providing diagnostic antibodies) or in vitro (e.g. by phage display technology or another technique useful for generating synthetic antibodies).

The invention provides vaccine formulations for the prevention and treatment of infections with SCoV-like virus. In certain embodiments, the vaccine of the invention comprises recombinant and chimeric viruses of the SCoV-like virus. In certain embodiments, the virus is attenuated.

In another embodiment of this aspect of the invention, inactivated vaccine formulations may be prepared using conventional techniques to "kill" the chimeric viruses. Inactivated vaccines are "dead" in the sense that their infectivity has been destroyed. Ideally, the infectivity of the virus is destroyed without affecting its immunogenicity. In order to prepare inactivated vaccines, the chimeric virus may be grown in cell culture or in the allantois of the chick embryo, purified by zonal ultracentrifugation, inactivated by formaldehyde or β -propiolactone, and pooled. The resulting vaccine is usually inoculated intramuscularly.

Inactivated viruses may be formulated with a suitable adjuvant in order to enhance the immunological response. Such adjuvants may include but are not limited to mineral gels, e.g., aluminum hydroxide; surface active substances such as lysolecithin, pluronic polyols, polyanions; peptides; oil emulsions; and potentially useful human adjuvants such as BCG and *Corynebacterium parvum*.

In another aspect, the present invention also provides DNA vaccine formulations comprising a nucleic acid or fragment of the SCoV-like virus, or nucleic acid molecules having the sequence of SEQ ID NO:1, 2, or 4, or a fragment thereof. In another specific embodiment, the DNA vaccine formulations of the present invention comprises a nucleic acid or fragment thereof encoding the antibodies which immunospecifically binds SCoV-like viruses. In DNA vaccine formulations, a vaccine DNA comprises a viral vector, such as that derived from the SCoV-like virus, bacterial plasmid, or other expression vector, bearing an insert comprising a nucleic acid molecule of the present invention operably linked to one or more control elements, thereby allowing expression of the vaccinating proteins encoded by said nucleic acid molecule in a vaccinated subject. Such vectors can be prepared by recombinant DNA technology as recombinant or chimeric viral vectors carrying a nucleic acid molecule of the present invention (see also Section 5.1, supra).

Various heterologous vectors are described for DNA vaccinations against viral infections. For example, the vectors described in the following references may be used to express SCoV-like viral sequences instead of the sequences

of the viruses or other pathogens described; in particular, vectors described for hepatitis B virus (Michel, M. L. et al., 1995, DNA-mediated immunization to the hepatitis B surface antigen in mice: Aspects of the humoral response mimic hepatitis B viral infection in humans, *Proc. Natl. Acad. Sci. USA* 92:5307-5311; Davis, H. L. et al., 1993, DNA-based immunization induces continuous secretion of hepatitis B surface antigen and high levels of circulating antibody, *Human Molec. Genetics* 2:1847-1851), HIV virus (Wang, B. et al., 1993, Gene inoculation generates immune responses against human immunodeficiency virus type 1, *Proc. Natl. Acad. Sci. USA* 90:4156-4160; Lu, S. et al., 1996, Simian immunodeficiency virus DNA vaccine trial in macaques, *J. Virol.* 70:3978-3991; Letvin, N. L. et al., 1997, Potent, protective anti-HIV immune responses generated by bimodal HIV envelope DNA plus protein vaccination, *Proc Natl Acad Sci USA*. 94(17):9378-83), and influenza viruses (Robinson, H L et al., 1993, Protection against a lethal influenza virus challenge by immunization with a haemagglutinin-expressing plasmid DNA, *Vaccine* 11:957-960; Ulmer, J. B. et al., Heterologous protection against influenza by injection of DNA encoding a viral protein, *Science* 259:1745-1749), as well as bacterial infections, such as tuberculosis (Tascon, R. E. et al., 1996, Vaccination against tuberculosis by DNA injection, *Nature Med.* 2:888-892; Huygen, K. et al., 1996, Immunogenicity and protective efficacy of a tuberculosis DNA vaccine, *Nature Med.*, 2:893-898), and parasitic infection, such as malaria (Sedegah, M., 1994, Protection against malaria by immunization with plasmid DNA encoding circumsporozoite protein, *Proc. Natl. Acad. Sci. USA* 91:9866-9870; Doolan, D. L. et al., 1996, Circumventing genetic restriction of protection against malaria with multigene DNA immunization: CD8+ T cell-interferon δ , and nitric oxide-dependent immunity, *J. Exper. Med.*, 1183:1739-1746).

Many methods may be used to introduce the vaccine formulations described above. These include, but are not limited to, oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, and intranasal routes. Alternatively, it may be preferable to introduce the chimeric virus vaccine formulation via the natural route of infection of the pathogen for which the vaccine is designed. The DNA vaccines of the present invention may be administered in saline solutions by injections into muscle or skin using a syringe and needle (Wolff J. A. et al., 1990, Direct gene transfer into mouse muscle in vivo, *Science* 247:1465-1468; Raz, E., 1994, Intradermal gene immunization: The possible role of DNA uptake in the induction of cellular immunity to viruses, *Proc. Natl. Acad. Sci. USA* 91:9519-9523). Another way to administer DNA vaccines is called "gene gun" method, whereby microscopic gold beads coated with the DNA molecules of interest is fired into the cells (Tang, D. et al., 1992, Genetic immunization is a simple method for eliciting an immune response, *Nature* 356:152-154). For general reviews of the methods for DNA vaccines, see Robinson, H. L., 1999, DNA vaccines: basic mechanism and immune responses (Review), *Int. J. Mol. Med.* 4(5):549-555; Barber, B., 1997, Introduction: Emerging vaccine strategies, *Seminars in Immunology* 9(5):269-270; and Robinson, H. L. et al., 1997, DNA vaccines, *Seminars in Immunology* 9(5):271-283.

5.3 Attenuation of SCoV-Like Virus or Variants Thereof

The SCoV-like virus or variants thereof of the invention can be genetically engineered to exhibit an attenuated phe-

notype. In particular, the viruses of the invention exhibit an attenuated phenotype in a subject to which the virus is administered as a vaccine. Attenuation can be achieved by any method known to a skilled artisan. Without being bound by theory, the attenuated phenotype of the viruses of the invention can be caused, e.g., by using a virus that naturally does not replicate well in an intended host species, for example, by reduced replication of the viral genome, by reduced ability of the virus to infect a host cell, or by reduced ability of the viral proteins to assemble to an infectious viral particle relative to the wild type strain of the virus.

The attenuated phenotypes of SCoV-like virus or variants thereof can be tested by any method known to the artisan. A candidate virus can, for example, be tested for its ability to infect a host or for the rate of replication in a cell culture system. In certain embodiments, growth curves at different temperatures are used to test the attenuated phenotype of the virus. For example, an attenuated virus is able to grow at 35° C., but not at 39° C. or 40° C. In certain embodiments, different cell lines can be used to evaluate the attenuated phenotype of the virus. For example, an attenuated virus may only be able to grow in monkey cell lines but not the human cell lines, or the achievable virus titers in different cell lines are different for the attenuated virus. In certain embodiments, viral replication in the respiratory tract of a small animal model, including but not limited to, hamsters, cotton rats, mice and guinea pigs, is used to evaluate the attenuated phenotypes of the virus. In other embodiments, the immune response induced by the virus, including but not limited to, the antibody titers (e.g., assayed by plaque reduction neutralization assay or ELISA) is used to evaluate the attenuated phenotypes of the virus. In a specific embodiment, the plaque reduction neutralization assay or ELISA is carried out at a low dose. In certain embodiments, the ability of the SCoV-like virus to elicit pathological symptoms in an animal model can be tested. A reduced ability of the virus to elicit pathological symptoms in an animal model system is indicative of its attenuated phenotype. In a specific embodiment, the candidate viruses are tested in a monkey model for nasal infection, indicated by mucous production.

The viruses of the invention can be attenuated such that one or more of the functional characteristics of the virus are impaired. In certain embodiments, attenuation is measured in comparison to the wild type strain of the virus from which the attenuated virus is derived. In other embodiments, attenuation is determined by comparing the growth of an attenuated virus in different host systems. Thus, for a non-limiting example, SCoV-like virus or a variant thereof is said to be attenuated when grown in a human host if the growth of the SCoV-like virus or variant thereof in the human host is reduced compared to the non-attenuated SCoV-like virus or variant thereof.

In certain embodiments, the attenuated virus of the invention is capable of infecting a host, is capable of replicating in a host such that infectious viral particles are produced. In comparison to the wild type strain, however, the attenuated strain grows to lower titers or grows more slowly. Any technique known to the skilled artisan can be used to determine the growth curve of the attenuated virus and compare it to the growth curve of the wild type virus.

In certain embodiments, the attenuated virus of the invention (e.g., a recombinant or chimeric SCoV-like virus) cannot replicate in human cells as well as the wild type virus (e.g., wild type SCoV-like virus) does. However, the attenuated virus can replicate well in a cell line that lack interferon functions, such as Vero cells.

In other embodiments, the attenuated virus of the invention is capable of infecting a host, of replicating in the host, and of causing proteins of the virus of the invention to be inserted into the cytoplasmic membrane, but the attenuated virus does not cause the host to produce new infectious viral particles. In certain embodiments, the attenuated virus infects the host, replicates in the host, and causes viral proteins to be inserted in the cytoplasmic membrane of the host with the same efficiency as the wild type SCoV-like virus. In other embodiments, the ability of the attenuated virus to cause viral proteins to be inserted into the cytoplasmic membrane into the host cell is reduced compared to the wild type virus. In certain embodiments, the ability of the attenuated SCoV-like virus to replicate in the host is reduced compared to the wild type virus. Any technique known to the skilled artisan can be used to determine whether a virus is capable of infecting a mammalian cell, of replicating within the host, and of causing viral proteins to be inserted into the cytoplasmic membrane of the host.

In certain embodiments, the attenuated virus of the invention is capable of infecting a host. In contrast to the wild type SCoV-like virus, however, the attenuated SCoV-like virus cannot be replicated in the host. In a specific embodiment, the attenuated SCoV-like virus can infect a host and can cause the host to insert viral proteins in its cytoplasmic membranes, but the attenuated virus is incapable of being replicated in the host. Any method known to the skilled artisan can be used to test whether the attenuated SCoV-like virus has infected the host and has caused the host to insert viral proteins in its cytoplasmic membranes.

In certain embodiments, the ability of the attenuated virus to infect a host is reduced compared to the ability of the wild type virus to infect the same host. Any technique known to the skilled artisan can be used to determine whether a virus is capable of infecting a host.

In certain embodiments, mutations (e.g., missense mutations) are introduced into the genome of the virus, for example, into the sequence of SEQ ID NO:1, 2, 4, or to generate a virus with an attenuated phenotype. Mutations (e.g., missense mutations) can be introduced into the structural genes and/or regulatory genes of the SCoV-like virus. Mutations can be additions, substitutions, deletions, or combinations thereof. Such variant of SCoV-like virus can be screened for a predicted functionality, such as infectivity, replication ability, protein synthesis ability, assembling ability, as well as cytopathic effect in cell cultures. In a specific embodiment, the missense mutation is a cold-sensitive mutation. In another embodiment, the missense mutation is a heat-sensitive mutation. In another embodiment, the missense mutation prevents a normal processing or cleavage of the viral proteins.

In other embodiments, deletions are introduced into the genome of the SCoV-like virus, which result in the attenuation of the virus.

In certain embodiments, attenuation of the virus is achieved by replacing a gene of the wild type virus with a gene of a virus of a different species, of a different subgroup, or of a different variant. In another aspect, attenuation of the virus is achieved by replacing one or more specific domains of a protein of the wild type virus with domains derived from the corresponding protein of a virus of a different species. In certain other embodiments, attenuation of the virus is achieved by deleting one or more specific domains of a protein of the wild type virus.

When a live attenuated vaccine is used, its safety must also be considered. The vaccine must not cause disease. Any techniques known in the art that can make a vaccine safe

may be used in the present invention. In addition to attenuation techniques, other techniques may be used. One non-limiting example is to use a soluble heterologous gene that cannot be incorporated into the virion membrane. For example, a single copy of the soluble version of a viral transmembrane protein lacking the transmembrane and cytosolic domains thereof, can be used.

Various assays can be used to test the safety of a vaccine. For example, sucrose gradients and neutralization assays can be used to test the safety. A sucrose gradient assay can be used to determine whether a heterologous protein is inserted in a virion. If the heterologous protein is inserted in the virion, the virion should be tested for its ability to cause symptoms in an appropriate animal model since the virus may have acquired new, possibly pathological, properties.

5.4 Adjuvants and Carrier Molecules

SCoV-like-viral-associated antigens are administered with one or more adjuvants.

In one embodiment, the SCoV-like-viral-associated antigen is administered together with a mineral salt adjuvants or mineral salt gel adjuvant. Such mineral salt and mineral salt gel adjuvants include, but are not limited to, aluminum hydroxide (ALHYDROGEL, REHYDRAGEL), aluminum phosphate gel, aluminum hydroxyphosphate (ADJUPHOS), and calcium phosphate.

In another embodiment, SCoV-like-viral-associated antigen is administered with an immunostimulatory adjuvant. Such class of adjuvants, include, but are not limited to, cytokines (e.g., interleukin-2, interleukin-7, interleukin-12, granulocyte-macrophage colony stimulating factor (GM-CSF), interferon- γ interleukin-1 β (IL-1 β), and IL-1 β peptide or Sclavo Peptide), cytokine-containing liposomes, triterpenoid glycosides or saponins (e.g., QuilA and QS-21, also sold under the trademark STIMULON, ISCOPREP), Muramyl Dipeptide (MDP) derivatives, such as N-acetylmuramyl-L-threonyl-D-isoglutamine (Threonyl-MDP, sold under the trademark TERMURTIDE), GMDP, N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine, N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxy phosphoryloxy)-ethylamine, muramyl tripeptide phosphatidylethanolamine (MTP-PE), unmethylated CpG dinucleotides and oligonucleotides, such as bacterial DNA and fragments thereof, LPS, monophosphoryl Lipid A (3D-MLA sold under the trademark MPL), and polyphosphazenes.

In another embodiment, the adjuvant used is a particular adjuvant, including, but not limited to, emulsions, e.g., Freund's Complete Adjuvant, Freund's Incomplete Adjuvant, squalene or squalane oil-in-water adjuvant formulations, such as SAF and MF59, e.g., prepared with block-copolymers, such as L-121 (polyoxypropylene/polyoxyethylene) sold under the trademark PLURONIC L-121, Liposomes, Virosomes, cochleates, and immune stimulating complex, which is sold under the trademark ISCOM.

In another embodiment, a microparticulate adjuvant is used. Microparticulate adjuvants include, but are not limited to biodegradable and biocompatible polyesters, homo- and copolymers of lactic acid (PLA) and glycolic acid (PGA), poly(lactide-co-glycolides) (PLGA) microparticles, polymers that self-associate into particulates (poloxamer particles), soluble polymers (polyphosphazenes), and virus-like particles (VLPs) such as recombinant protein particulates, e.g., hepatitis B surface antigen (HbsAg).

Yet another class of adjuvants that may be used include mucosal adjuvants, including but not limited to heat-labile enterotoxin from *Escherichia coli* (LT), cholera holotoxin (CT) and cholera Toxin B Subunit (CTB) from *Vibrio cholerae*, mutant toxins (e.g., LTK63 and LTR72), microparticles, and polymerized liposomes.

In other embodiments, any of the above classes of adjuvants may be used in combination with each other or with other adjuvants. For example, non-limiting examples of combination adjuvant preparations that can be used to administer the SCoV-like-viral-associated antigens of the invention include liposomes containing immunostimulatory protein, cytokines, or T-cell and/or B-cell peptides, or microbes with or without entrapped IL-2 or microparticles containing enterotoxin. Other adjuvants known in the art are also included within the scope of the invention (see *Vaccine Design: The Subunit and Adjuvant Approach*, Chap. 7, Michael F. Powell and Mark J. Newman (eds.), Plenum Press, New York, 1995, which is incorporated herein in its entirety).

The effectiveness of an adjuvant may be determined by measuring the induction of antibodies directed against an immunogenic polypeptide containing a SCoV-like viral polypeptide epitope, the antibodies resulting from administration of this polypeptide in vaccines which are also comprised of the various adjuvants.

The polypeptides may be formulated into the vaccine as neutral or salt forms. Pharmaceutically acceptable salts include the acid additional salts (formed with free amino groups of the peptide) and which are formed with inorganic acids, such as, for example, hydrochloric or phosphoric acids, or organic acids such as acetic, oxalic, tartaric, maleic, and the like. Salts formed with free carboxyl groups may also be derived from inorganic bases, such as, for example, sodium potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine and the like.

The vaccines of the invention may be multivalent or univalent. Multivalent vaccines are made from recombinant viruses that direct the expression of more than one antigen.

Many methods may be used to introduce the vaccine formulations of the invention; these include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal routes, and via scarification (scratching through the top layers of skin, e.g., using a bifurcated needle).

The patient to which the vaccine is administered is preferably a mammal, most preferably a human, but can also be a non-human animal including but not limited to cows, horses, sheep, pigs, fowl (e.g., chickens), goats, cats, dogs, hamsters, mice and rats.

5.5 Preparation of Antibodies

Antibodies which specifically recognize a polypeptide of the invention, such as, but not limited to, polypeptides comprising the sequence of SEQ ID NO:3, and polypeptides as shown in FIGS. 4, 5, and 7, or SCoV-like viral epitope or antigen-binding fragments thereof can be used for detecting, screening, and isolating the polypeptide of the invention or fragments thereof, or similar sequences that might encode similar enzymes from the other organisms. For example, in one specific embodiment, an antibody which immunospecifically binds SCoV-like viral epitope, or a fragment thereof, can be used for various in vitro detection assays, including enzyme-linked immunosorbent assays (ELISA),

radioimmunoassays, Western blot, etc., for the detection of a polypeptide of the invention or, preferably, SCoV-like virus, in samples, for example, a biological material, including cells, cell culture media (e.g., bacterial cell culture media, mammalian cell culture media, insect cell culture media, yeast cell culture media, etc.), blood, plasma, serum, tissues, sputum, nasopharyngeal aspirates, etc.

Antibodies specific for a polypeptide of the invention or any epitope of SCoV-like virus may be generated by any suitable method known in the art. Polyclonal antibodies to an antigen-of-interest, for example, the SCoV-like virus or comprises a nucleic acid sequence of SEQ ID NO:1, 2, or 4 can be produced by various procedures well known in the art. For example, an antigen can be administered to various host animals including, but not limited to, rabbits, mice, rats, etc., to induce the production of antisera containing polyclonal antibodies specific for the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species, and include but are not limited to, Freund's (complete and incomplete) adjuvant, mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful adjuvants for humans such as BCG (Bacille Calmette-Guerin) and *Corynebacterium parvum*. Such adjuvants are also well known in the art.

Monoclonal antibodies can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display technologies, or a combination thereof. For example, monoclonal antibodies can be produced using hybridoma techniques including those known in the art and taught, for example, in Harlow et al., *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: *Monoclonal Antibodies and T-Cell Hybridomas*, pp. 563-681 (Elsevier, N.Y., 1981) (both of which are incorporated by reference in their entireties). The term "monoclonal antibody" as used herein is not limited to antibodies produced through hybridoma technology. The term "monoclonal antibody" refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

Methods for producing and screening for specific antibodies using hybridoma technology are routine and well known in the art. In a non-limiting example, mice can be immunized with an antigen of interest or a cell expressing such an antigen. Once an immune response is detected, e.g., antibodies specific for the antigen are detected in the mouse serum, the mouse spleen is harvested and splenocytes isolated. The splenocytes are then fused by well known techniques to any suitable myeloma cells. Hybridomas are selected and cloned by limiting dilution. The hybridoma clones are then assayed by methods known in the art for cells that secrete antibodies capable of binding the antigen. Ascites fluid, which generally contains high levels of antibodies, can be generated by inoculating mice intraperitoneally with positive hybridoma clones.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, Fab and F(ab')₂ fragments may be produced by proteolytic cleavage of immunoglobulin molecules, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). F(ab')₂ fragments contain the complete light chain, and the variable region, the CH1 region and the hinge region of the heavy chain.

The antibodies of the invention or fragments thereof can be also produced by any method known in the art for the

synthesis of antibodies, in particular, by chemical synthesis or preferably, by recombinant expression techniques.

The nucleotide sequence encoding an antibody may be obtained from any information available to those skilled in the art (i.e., from Genbank, the literature, or by routine cloning and sequence analysis). If a clone containing a nucleic acid encoding a particular antibody or an epitope-binding fragment thereof is not available, but the sequence of the antibody molecule or epitope-binding fragment thereof is known, a nucleic acid encoding the immunoglobulin may be chemically synthesized or obtained from a suitable source (e.g., an antibody cDNA library, or a cDNA library generated from, or nucleic acid, preferably poly A+ RNA, isolated from any tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe specific for the particular gene sequence to identify, e.g., a cDNA clone from a cDNA library that encodes the antibody. Amplified nucleic acids generated by PCR may then be cloned into replicable cloning vectors using any method well known in the art.

Once the nucleotide sequence of the antibody is determined, the nucleotide sequence of the antibody may be manipulated using methods well known in the art for the manipulation of nucleotide sequences, e.g., recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al., supra; and Ausubel et al., eds., 1998, *Current Protocols in Molecular Biology*, John Wiley & Sons, NY, which are both incorporated by reference herein in their entireties), to generate antibodies having a different amino acid sequence by, for example, introducing amino acid substitutions, deletions, and/or insertions into the epitope-binding domain regions of the antibodies or any portion of antibodies which may enhance or reduce biological activities of the antibodies.

Recombinant expression of an antibody requires construction of an expression vector containing a nucleotide sequence that encodes the antibody. Once a nucleotide sequence encoding an antibody molecule or a heavy or light chain of an antibody, or portion thereof has been obtained, the vector for the production of the antibody molecule may be produced by recombinant DNA technology using techniques well known in the art as discussed in the previous sections. Methods which are well known to those skilled in the art can be used to construct expression vectors containing antibody coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. The nucleotide sequence encoding the heavy-chain variable region, light-chain variable region, both the heavy-chain and light-chain variable regions, an epitope-binding fragment of the heavy- and/or light-chain variable region, or one or more complementarity determining regions (CDRs) of an antibody may be cloned into such a vector for expression. Thus-prepared expression vector can be then introduced into appropriate host cells for the expression of the antibody. Accordingly, the invention includes host cells containing a polynucleotide encoding an antibody specific for the polypeptides of the invention or fragments thereof.

The host cell may be co-transfected with two expression vectors of the invention, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors may con-

tain identical selectable markers which enable equal expression of heavy and light chain polypeptides or different selectable markers to ensure maintenance of both plasmids. Alternatively, a single vector may be used which encodes, and is capable of expressing, both heavy and light chain polypeptides. In such situations, the light chain should be placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot, *Nature*, 322:52, 1986; and Kohler, *Proc. Natl. Acad. Sci. USA*, 77:2 197, 1980). The coding sequences for the heavy and light chains may comprise cDNA or genomic DNA.

In another embodiment, antibodies can also be generated using various phage display methods known in the art. In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. In a particular embodiment, such phage can be utilized to display antigen binding domains, such as Fab and Fv or disulfide-bond stabilized Fv, expressed from a repertoire or combinatorial antibody library (e.g., human or murine). Phage expressing an antigen binding domain that binds the antigen of interest can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured to a solid surface or bead. Phage used in these methods are typically filamentous phage, including fd and M13. The antigen binding domains are expressed as a recombinantly fused protein to either the phage gene III or gene VIII protein. Examples of phage display methods that can be used to make the immunoglobulins, or fragments thereof, of the present invention include those disclosed in Brinkman et al., *J. Immunol. Methods*, 182:41-50, 1995; Ames et al., *J. Immunol. Methods*, 184: 177-186, 1995; Kettleborough et al., *Eur. J. Immunol.*, 24:952-958, 1994; Persic et al., *Gene*, 187:9-18, 1997; Burton et al., *Advances in Immunology*, 57:191-280, 1994; PCT application No. PCT/GB91/01134; PCT publications WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and U.S. Pat. Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired fragments, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as described in detail below. For example, techniques to recombinantly produce Fab, Fab' and F(ab')₂ fragments can also be employed using methods known in the art such as those disclosed in PCT publication WO 92/22324; Mullinax et al., *BioTechniques*, 12(6):864-869, 1992; and Sawai et al., *AJRI*, 34:26-34, 1995; and Better et al., *Science*, 240:1041-1043, 1988 (each of which is incorporated by reference in its entirety). Examples of techniques which can be used to produce single-chain Fvs and antibodies include those described in U.S. Pat. Nos. 4,946,778 and 5,258,498; Huston et al., *Methods in Enzymology*, 203:46-88, 1991; Shu et al., *PNAS*, 90:7995-7999, 1993; and Skerra et al., *Science*, 240:1038-1040, 1988.

Once an antibody molecule of the invention has been produced by any methods described above, it may then be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for the specific antigen after Protein A or Protein G purification,

and sizing column chromatography), centrifugation, differential solubility, or by any other standard techniques for the purification of proteins. Further, the antibodies of the present invention or fragments thereof may be fused to heterologous polypeptide sequences described herein or otherwise known in the art to facilitate purification.

For some uses, including in vivo use of antibodies in humans and in vitro detection assays, it may be preferable to use chimeric, humanized, or human antibodies. A chimeric antibody is a molecule in which different portions of the antibody are derived from different animal species, such as antibodies having a variable region derived from a murine monoclonal antibody and a constant region derived from a human immunoglobulin. Methods for producing chimeric antibodies are known in the art. See e.g., Morrison, *Science*, 229:1202, 1985; Oi et al., *BioTechniques*, 4:214 1986; Gillies et al., *J. Immunol. Methods*, 125:191-202, 1989; U.S. Pat. Nos. 5,807,715; 4,816,567; and 4,816,397, which are incorporated herein by reference in their entireties. Humanized antibodies are antibody molecules from non-human species that bind the desired antigen having one or more complementarity determining regions (CDRs) from the non-human species and framework regions from a human immunoglobulin molecule. Often, framework residues in the human framework regions will be substituted with the corresponding residue from the CDR donor antibody to alter, preferably improve, antigen binding. These framework substitutions are identified by methods well known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important for antigen binding and sequence comparison to identify unusual framework residues at particular positions. See, e.g., Queen et al., U.S. Pat. No. 5,585,089; Riechmann et al., *Nature*, 332:323, 1988, which are incorporated herein by reference in their entireties. Antibodies can be humanized using a variety of techniques known in the art including, for example, CDR-grafting (EP 239,400; PCT publication WO 91/09967; U.S. Pat. Nos. 5,225,539; 5,530,101 and 5,585,089), veneering or resurfacing (EP 592,106; EP 519,596; Padlan, *Molecular Immunology*, 28(4/5):489-498, 1991; Studnicka et al., *Protein Engineering*, 7(6):805-814, 1994; Roguska et al., *Proc Natl. Acad. Sci. USA*, 91:969-973, 1994), and chain shuffling (U.S. Pat. No. 5,565,332), all of which are hereby incorporated by reference in their entireties.

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Human antibodies can be made by a variety of methods known in the art including phage display methods described above using antibody libraries derived from human immunoglobulin sequences. See U.S. Pat. Nos. 4,444,887 and 4,716,111; and PCT publications WO 98/46645; WO 98/50433; WO 98/24893; WO 98/16654; WO 96/34096; WO 96/33735; and WO 91/10741, each of which is incorporated herein by reference in its entirety.

Human antibodies can also be produced using transgenic mice which are incapable of expressing functional endogenous immunoglobulins, but which can express human immunoglobulin genes. For an overview of this technology for producing human antibodies, see Lonberg and Huszar, *Int. Rev. Immunol.*, 13:65-93, 1995. For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; European Patent No. 0 598 877; U.S. Pat. Nos. 5,413,923; 5,625,126; 5,633,425; 5,569,825; 5,661,016; 5,545,806; 5,814,318;

5,885,793; 5,916,771; and 5,939,598, which are incorporated by reference herein in their entireties. In addition, companies such as Abgenix, Inc. (Fremont, Calif.), Medarex (NJ) and Genpharm (San Jose, Calif.) can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al., *Bio/technology*, 12:899-903, 1988).

Antibodies fused or conjugated to heterologous polypeptides may be used in in vitro immunoassays and in purification methods (e.g., affinity chromatography) well known in the art. See e.g., PCT publication Number WO 93/21232; EP 439,095; Naramura et al., *Immunol. Lett.*, 39:91-99, 1994; U.S. Pat. No. 5,474,981; Gillies et al., *PNAS*, 89:1428-1432, 1992; and Fell et al., *J. Immunol.*, 146:2446-2452, 1991, which are incorporated herein by reference in their entireties.

Antibodies may also be attached to solid supports, which are particularly useful for immunoassays or purification of the polypeptides of the invention or fragments, derivatives, analogs, or variants thereof, or similar molecules having the similar enzymatic activities as the polypeptide of the invention. Such solid supports include, but are not limited to, glass, cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene.

5.6 Pharmaceutical Compositions and Kits

The present invention encompasses pharmaceutical compositions comprising anti-viral agents of the present invention. In a specific embodiment, the anti-viral agent is an antibody which immunospecifically binds and neutralize the SCoV-like virus or variants thereof, or any proteins derived therefrom. In another specific embodiment, the anti-viral agent is a polypeptide or nucleic acid molecule of the invention. The pharmaceutical compositions have utility as an anti-viral prophylactic agent and may be administered to a subject where the subject has been exposed or is expected to be exposed to a virus.

Various delivery systems are known and can be used to administer the pharmaceutical composition of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the mutant viruses, receptor mediated endocytosis (see, e.g., Wu and Wu, 1987, *J. Biol. Chem.* 262:4429-4432). Methods of introduction include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The compounds may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local. In a preferred embodiment, it may be desirable to introduce the pharmaceutical compositions of the invention into the lungs by any suitable route. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compositions of the invention locally to the area in need of treatment; this may be achieved

by, for example, and not by way of limitation, local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. In one embodiment, administration can be by direct injection at the site (or former site) infected tissues.

In another embodiment, the pharmaceutical composition can be delivered in a vesicle, in particular a liposome (see Langer, 1990, *Science* 249:1527-1533; Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez Berestein and Fidler (eds.), Liss, New York, pp. 353-365 (1989); Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*).

In yet another embodiment, the pharmaceutical composition can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, *supra*; Sefton, 1987, *CRC Crit. Ref. Biomed. Eng.* 14:201; Buchwald et al., 1980, *Surgery* 88:507; and Saudek et al., 1989, *N. Engl. J. Med.* 321:574). In another embodiment, polymeric materials can be used (see *Medical Applications of Controlled Release*, Langer and Wise (eds.), CRC Press, Boca Raton, Fla. (1974); *Controlled Drug Bioavailability, Drug Product Design and Performance*, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, *J. Macromol. Sci. Rev. Macromol. Chem.* 23:61 (1983); see also Levy et al., 1985, *Science* 228:190; During et al., 1989, *Ann. Neurol.* 25:351; Howard et al., 1989, *J. Neurosurg.* 71:105). In yet another embodiment, a controlled release system can be placed in proximity of the composition's target, i.e., the lung, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in *Medical Applications of Controlled Release*, *supra*, vol. 2, pp. 115-138 (1984)).

Other controlled release systems are discussed in the review by Langer (*Science* 249:1527-1533 (1990)).

The pharmaceutical compositions of the present invention comprise a therapeutically effective amount of an live attenuated, inactivated or killed SCoV-like virus, or recombinant or chimeric SCoV-like virus, and a pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the pharmaceutical composition is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can

include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E. W. Martin. The formulation should suit the mode of administration.

In a preferred embodiment, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

The pharmaceutical compositions of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with free carboxyl groups such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2 ethylamino ethanol, histidine, procaine, etc.

The amount of the pharmaceutical composition of the invention which will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. However, suitable dosage ranges for intravenous administration are generally about 20-500 micrograms of active compound per kilogram body weight. Suitable dosage ranges for intranasal administration are generally about 0.01 pg/kg body weight to 1 mg/kg body weight. Effective doses may be extrapolated from dose response curves derived from in vitro or animal model test systems.

Suppositories generally contain active ingredient in the range of 0.5% to 10% by weight; oral formulations preferably contain 10% to 95% active ingredient.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In a preferred embodiment, the kit contains an antiviral agent of the invention, e.g., an antibody specific for the polypeptides encoded by a nucleotide sequence of SEQ ID NO:1, 2 or 4, or as shown in FIGS. 4, 5 and 7, or any SCoV-like viral epitope, or a polypeptide or protein of the

present invention, or a nucleic acid molecule of the invention, alone or in combination with adjuvants, antivirals, antibiotics, analgesic, bronchodilators, or other pharmaceutically acceptable excipients.

The present invention further encompasses kits comprising a container containing a pharmaceutical composition of the present invention and instructions to for use.

5.7 Detection Assays

An exemplary method for detecting the presence or absence of a polypeptide or nucleic acid of the invention in a biological sample involves obtaining a biological sample from various sources and contacting the sample with a compound or an agent capable of detecting an epitope or nucleic acid (e.g., mRNA, genomic DNA) of the SCoV-like virus such that the presence of the SCoV-like virus is detected in the sample. A preferred agent for detecting SCoV-like viral mRNA or genomic RNA of the invention is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic RNA encoding a polypeptide of the invention. The nucleic acid probe can be, for example, a nucleic acid molecule comprising or consisting of the nucleotide sequence or SEQ ID NO:1, 2, 4, or a portion thereof, such as an oligonucleotide of at least 15, 20, 25, 30, 50, 100, 250, 500, 750, 1,000 or more contiguous nucleotides in length and sufficient to specifically hybridize under stringent conditions to a SCoV-like viral mRNA or genomic RNA.

In another preferred specific embodiment, the presence of SCoV-like virus is detected in the sample by an reverse transcription polymerase chain reaction (RT-PCR) using the primers that are constructed based on a partial nucleotide sequence of the genome of SCoV-like virus. In a non-limiting specific embodiment, preferred primers to be used in a RT-PCR method comprises SEQ ID NO:5 and/or 6 in the presence of 2.5 mM MgCl₂ and the thermal cycles are, for example, but not limited to, 94° C. for 8 min followed by 40 cycles of 94° C. for 1 min, 50° C. for 1 min, 72° C. for 1 min. In more preferred specific embodiment, the present invention provides a real-time quantitative PCR assay to detect the presence of SCoV-like virus in a biological sample by subjecting the cDNA obtained by reverse transcription of the extracted total RNA from the sample to PCR reactions using the specific primers, such as those having nucleotide sequences of SEQ ID NOS:5 and/or 6, and a fluorescence dye, such as SYBR® Green I, which fluoresces when bound non-specifically to double-stranded DNA. The fluorescence signals from these reactions are captured at the end of extension steps as PCR product is generated over a range of the thermal cycles, thereby allowing the quantitative determination of the viral load in the sample based on an amplification plot.

A preferred agent for detecting SCoV-like virus is an antibody that specifically binds a polypeptide of the invention or any SCoV-like viral epitope, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., Fab or F(ab')₂) can be used.

The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluores-

cently labeled streptavidin. The detection method of the invention can be used to detect mRNA, protein (or any epitope), or genomic RNA in a sample in vitro as well as in vivo. For example, in vitro techniques for detection of mRNA include northern hybridizations, in situ hybridizations, RT-PCR, and RNase protection. In vitro techniques for detection of an epitope of SCoV-like virus include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. In vitro techniques for detection of genomic RNA include northern hybridizations, RT-PCT, and RNase protection. Furthermore, in vivo techniques for detection of SCoV-like virus include introducing into a subject organism a labeled antibody directed against the polypeptide. For example, the antibody can be labeled with a radioactive marker whose presence and location in the subject organism can be detected by standard imaging techniques, including autoradiography.

In a specific embodiment, the methods further involve obtaining a control sample from a control subject, contacting the control sample with a compound or agent capable of detecting SCoV-like virus, e.g., a polypeptide of the invention or mRNA or genomic RNA encoding a polypeptide of the invention, such that the presence of SCoV-like virus or the polypeptide or mRNA or genomic RNA encoding the polypeptide is detected in the sample, and comparing the presence of SCoV-like virus or the polypeptide or mRNA or genomic RNA encoding the polypeptide in the control sample with the presence of SCoV-like virus, or the polypeptide or mRNA or genomic DNA encoding the polypeptide in the test sample.

The invention also encompasses kits for detecting the presence of SCoV-like virus or a polypeptide or nucleic acid of the invention in a test sample. The kit, for example, can comprise a labeled compound or agent capable of detecting SCoV-like virus or the polypeptide or a nucleic acid molecule encoding the polypeptide in a test sample and, in certain embodiments, a means for determining the amount of the polypeptide or mRNA in the sample (e.g., an antibody which binds the polypeptide or an oligonucleotide probe which binds to DNA or mRNA encoding the polypeptide). Kits can also include instructions for use.

For antibody-based kits, the kit can comprise, for example: (1) a first antibody (e.g., attached to a solid support) which binds to a polypeptide of the invention or SCoV-like viral epitope; and, optionally, (2) a second, different antibody which binds to either the polypeptide or the first antibody and is conjugated to a detectable agent.

For oligonucleotide-based kits, the kit can comprise, for example: (1) an oligonucleotide, e.g., a detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a polypeptide of the invention or to a sequence within the SCoV-like viral genome or (2) a pair of primers useful for amplifying a nucleic acid molecule containing an SCoV-like viral sequence. The kit can also comprise, e.g., a buffering agent, a preservative, or a protein stabilizing agent. The kit can also comprise components necessary for detecting the detectable agent (e.g., an enzyme or a substrate). The kit can also contain a control sample or a series of control samples which can be assayed and compared to the test sample contained. Each component of the kit is usually enclosed within an individual container and all of the various containers are within a single package along with instructions for use.

5.8 Screening Assays to Identify Anti-Viral Agents

The invention provides methods for the identification of a compound that inhibits the ability of SCoV-like virus to infect a host or a host cell. In certain embodiments, the invention provides methods for the identification of a compound that reduces the ability of SCoV-like virus to replicate in a host or a host cell. Any technique well-known to the skilled artisan can be used to screen for a compound that would abolish or reduce the ability of SCoV-like virus to infect a host and/or to replicate in a host or a host cell.

In certain embodiments, the invention provides methods for the identification of a compound that inhibits the ability of SCoV-like virus to replicate in a mammal or a mammalian cell. More specifically, the invention provides methods for the identification of a compound that inhibits the ability of SCoV-like virus to infect a mammal or a mammalian cell. In certain embodiments, the invention provides methods for the identification of a compound that inhibits the ability of SCoV-like virus to replicate in a mammalian cell. In a specific embodiment, the mammalian cell is a human cell.

In another embodiment, a cell is contacted with a test compound and infected with the SCoV-like virus. In certain embodiments, a control culture is infected with the SCoV-like virus in the absence of a test compound. The cell can be contacted with a test compound before, concurrently with, or subsequent to the infection with the SCoV-like virus. In a specific embodiment, the cell is a mammalian cell. In an even more specific embodiment, the cell is a human cell. In certain embodiments, the cell is incubated with the test compound for at least 1 minute, at least 5 minutes at least 15 minutes, at least 30 minutes, at least 1 hour, at least 2 hours, at least 5 hours, at least 12 hours, or at least 1 day. The titer of the virus can be measured at any time during the assay. In certain embodiments, a time course of viral growth in the culture is determined. If the viral growth is inhibited or reduced in the presence of the test compound, the test compound is identified as being effective in inhibiting or reducing the growth or infection of the SCoV-like virus. In a specific embodiment, the compound that inhibits or reduces the growth of the SCoV-like virus is tested for its ability to inhibit or reduce the growth rate of other viruses to test its specificity for the SCoV-like virus.

In one embodiment, a test compound is administered to a model animal and the model animal is infected with the SCoV-like virus. In certain embodiments, a control model animal is infected with the SCoV-like virus without the administration of a test compound. The test compound can be administered before, concurrently with, or subsequent to the infection with the SCoV-like virus. In a specific embodiment, the model animal is a mammal. In an even more specific embodiment, the model animal can be, but is not limited to, a cotton rat, a mouse, or a monkey. The titer of the virus in the model animal can be measured at any time during the assay. In certain embodiments, a time course of viral growth in the culture is determined. If the viral growth is inhibited or reduced in the presence of the test compound, the test compound is identified as being effective in inhibiting or reducing the growth or infection of the SCoV-like virus. In a specific embodiment, the compound that inhibits or reduces the growth of the SCoV-like virus in the model animal is tested for its ability to inhibit or reduce the growth rate of other viruses to test its specificity for the SCoV-like virus.

The following examples illustrate the isolation and identification of the novel hSARS virus. These examples should not be construed as limiting.

6.1 Materials and Methods

6.1.1 Sampling

Specimens were collected at a main food retail market, Dongmen Market, in Shenzhen, Guangdong Province. Nasal and faecal swabs were taken for each examined animal and blood was taken wherever possible. After collection, all swabs were kept in virus transport medium (Medium199) with antibiotics.

6.1.2 Virus Isolation and RT-PCR Diagnostic Test

Nasal and faecal swabs were screened by RT-PCR using a pair primers designed to amplify the N gene of SCoV

Forward primer 5'-CAGCCCCAGATGGTACTTC-3' (SEQ ID NO:5)

Reverse primer 5'-TCTGCTTCCCTCTGCGTAC-3' (SEQ ID NO:6)

Nasal and faecal samples were cultured on faecal rhesus kidney (FRhK-4) cells for virus isolation as described. Peiris et al., 2003, *Lancet* 361:1319. Virus isolates were identified by RT-PCR followed by sequencing.

6.1.3 Neutralisation Assay

Animal sera were heat inactivated (56° C. for 30 minutes) and serially diluted from 1:20 to 1:640 and then mixed with 100 TCID₅₀ of the animal SCoV-like virus isolate SZ16. After incubation for 1 hour at 37° C., the mixture was inoculated in triplicate on to 96-well plates of FRhK-4 cell cultures. The results were read after 3 days incubation at 37° C.

6.1.4 Genetic Analysis

Viral RNA was extracted from the filtered supernatant of virus-infected FRhK-4 cells with the RNesay Mini Kit (Qiagen, Chatsworth, Calif.). A primer (5'-TTT TTT TTT TTT TTT GTG ATT-3') (SEQ ID NO:7) was designed for reverse transcription of viral RNA. Subsequently, polymerase chain reactions (PCR) were carried out using a series of primers prepared in our laboratory.

After purification of PCR products, cycling sequencing reactions were carried out to determine nucleotide sequence as reported. Guan et al., 2002, *Proc. Natl. Acad. Sci. U.S.A.* 99:8950. All sequence data were translated and analysed by Wisconsin Software Package, Version 10.1 (GCG). Phylogenetic relationship was determined using Clustal X 1.81 (Thompson et al., 1994, *Nucleic Acids Res.* 22:4673) and trees generated using Neighboring-Joining algorithms within PAUP, Version 4.0 (Genetics Computer Group, Madison, Wis.). Bootstrap scores are percentages out of 1000 replicates. Similar tree topologies were seen with Maximum Parsimony analysis.

The isolation and identification of SCoV like viruses from animals has now confirmed the hypothesis that SCoV is of animal origin. Both phylogenetic and sequence analysis of SCoV-like viruses suggest that these animal viruses are closely related to human SCoV isolated in the early stage of SARS outbreak. These animal species are either the natural reservoir of SCoV, or an intermediate host that is important in its transmission of the virus to humans. There is a role of the Raccoon-dog in the ecology of these viruses and that the Raccoon-dog may be the reservoir or they themselves may have acquired it from other sources such as a palm civets.

The factors associated with the emergence of novel infectious diseases are diverse and include human population growth and mobility, global transportation, urban crowding, agriculture practice changes and rapid virus evolution. Holland et al., 1991, *J. Virol.* 65:1960; Domingo et al., 1997, *Med Virol* 7:87. The emergence of human H5N1 influenza viruses in 1997 (Jong et al., 1997, *Nature* 389:544; Subbarao et al., 1998, *Science* 279:393) and early 2003 (author unpublished data) were good examples to highlight some of these factors. The emergence of SARS in humans is another, even more dramatic example of this. Exotic animals wild caught or farmed meeting culinary demand may be a continued source of introduction of this SCoV to humans. The present invention will help to better understand the inter-species transmission events that lead to the SARS outbreak.

Both H5N1 influenza and SARS emerged in the hypothetical pandemic influenza epicenter of southern China. Shortridge et al., 1982, *Lancet* ii:812; Guan et al., 2002, *Proc. Natl. Acad. Sci. U.S.A.* 99:8950. In the case of H5N1, chickens were the immediate source of virus for humans (Shortridge et al., 1998, *Virology* 252:331) and the depopulation of chicken in the live poultry markets and farms in Hong Kong resulted in the interruption of the outbreak and possibly averted an influenza pandemic in humans. However, nearly half year since the emergence of SARS, the precursor SCoV-like viruses are still simmering in food markets of southern China. Thus the recognition of SCoV-like viruses in animals is of pivotal significance in the control of SARS. An immediate ban of wild-animal trading for food or other use is of the highest priority in the global fight against SARS.

7. EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain many equivalents to the specific embodiments of the invention described herein using no more than routine experimentation. Such equivalents are intended to be encompassed by the following claims.

All publications, patents and patent applications mentioned in this specification are herein incorporated by reference into the specification to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated herein by reference.

Citation or discussion of a reference herein shall not be construed as an admission that such is prior art to the present invention.

SEQUENCE LISTING

The patent contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (<http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US07361747B2>). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed is:

1. An isolated nucleic acid molecule consisting of at least 12 contiguous nucleotides of the nucleotide sequence of SEQ ID NO:1, or the full-length complement thereof.
2. The nucleic acid molecule of claim 1, wherein the molecule is RNA.
3. The nucleic acid molecule of claim 1, wherein the molecule is DNA.
4. A vector consisting of at least 12 contiguous nucleotides of the nucleotide sequence of SEQ ID NO:1 operably linked to one or more control elements.
5. An isolated host cell comprising the vector of claim 4.

* * * * *